



#8

## SEQUENCE LISTING

<110> Haas, Rainer  
Kleanthous, Harold  
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Miller, Charles  
Al-Garawi, Amal  
Odenbreit, Stefan  
Meyer, Thomas

<120> Helicobacter Polypeptides and  
Corresponding Polynucleotide Molecules

<130> 06132/040002

<140> US 09/988,067

<141> 2001-11-16

<150> US 08/831,309

<151> 1997-04-01

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Met Lys Phe Leu Arg Ser Val Tyr Ala Phe Cys Ser Ser  
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tgg gta ggg acg att gtt att gtg ctg ttg gtt atc ttt ttt atc gcg 157  
Trp Val Gly Thr Ile Val Ile Val Leu Leu Val Ile Phe Phe Ile Ala  
15 20 25

caa gcc ttt atc att ccc tct cgc tct atg gtt ggc acg ctc tat gag 205  
Gln Ala Phe Ile Ile Pro Ser Arg Ser Met Val Gly Thr Leu Tyr Glu  
30 35 40 45

ggc gac atg ctc ttt gtc aaa aag ttt tct tac ggc ata ccc att cct 253  
Gly Asp Met Leu Phe Val Lys Lys Phe Ser Tyr Gly Ile Pro Ile Pro  
50 55 60

aaa atc cca tgg att gag ctt cct gtt atg cct gat ttt aaa aat aac 301  
Lys Ile Pro Trp Ile Glu Leu Pro Val Met Pro Asp Phe Lys Asn Asn  
65 70 75

gga cat ttg ata gag ggg gat cgc cct aag cgt ggc gaa gtg gtg gtg	349
Gly His Leu Ile Glu Gly Asp Arg Pro Lys Arg Gly Glu Val Val Val	
80 85 90	
ttt atc cct ccc cat gaa aaa aag tct tac tat gtt aaa agg aat ttt	397
Phe Ile Pro Pro His Glu Lys Lys Ser Tyr Tyr Val Lys Arg Asn Phe	
95 100 105	
gcc att gga ggc gat gag gtg ttg ttc act aat gag ggt ttt tat ttg	445
Ala Ile Gly Gly Asp Glu Val Leu Phe Thr Asn Glu Gly Phe Tyr Leu	
110 115 120 125	
cac cct ttt gag agc gac acg gac aaa aat tac atc gct aaa cat tac	493
His Pro Phe Glu Ser Asp Thr Asp Lys Asn Tyr Ile Ala Lys His Tyr	
130 135 140	
cct aac gcc atg aca aaa gaa ttt atg ggt aaa att ttt gtt tta aac	541
Pro Asn Ala Met Thr Lys Glu Phe Met Gly Lys Ile Phe Val Leu Asn	
145 150 155	
cct tat aaa aat gag cat ccg ggt atc cat tac caa aaa gac aat gaa	589
Pro Tyr Lys Asn Glu His Pro Gly Ile His Tyr Gln Lys Asp Asn Glu	
160 165 170	
acc ttc cac tta atg gag caa tta gcc act caa ggc gca gaa gct aat	637
Thr Phe His Leu Met Glu Gln Leu Ala Thr Gln Gly Ala Glu Ala Asn	
175 180 185	
atc agc atg caa ctc att caa atg gag ggc gaa aag gtg ttt tat aag	685
Ile Ser Met Gln Leu Ile Gln Met Glu Gly Glu Lys Val Phe Tyr Lys	
190 195 200 205	
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Lys Ile Asn Asp Asp Glu Phe Phe Met Ile Gly Asp Asn Arg Asp Asn	
210 215 220	
tct agc gac tcg cgc ttt tgg ggg agt gtg gct tat aaa aac atc gtg	781
Ser Ser Asp Ser Arg Phe Trp Gly Ser Val Ala Tyr Lys Asn Ile Val	
225 230 235	
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Gly Ser Pro Trp Phe Val Tyr Phe Ser Leu Ser Leu Lys Asn Ser Leu	
240 245 250	
gaa atg gat gca gaa aat aac cct aaa aaa cgc tat ctg gtg cgt tgg	877
Glu Met Asp Ala Glu Asn Asn Pro Lys Lys Arg Tyr Leu Val Arg Trp	
255 260 265	
gaa cgc atg ttt aaa agc gtt gga ggc tta gaa aaa atc att aaa aaa	925
Glu Arg Met Phe Lys Ser Val Gly Gly Leu Glu Lys Ile Ile Lys Lys	
270 275 280 285	
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 35 40 45  
 Leu Phe Val Lys Lys Phe Ser Tyr Gly Ile Pro Ile Pro Lys Ile Pro  
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 Trp Ile Glu Leu Pro Val Met Pro Asp Phe Lys Asn Asn Gly His Leu  
 65 70 75 80  
 Ile Glu Gly Asp Arg Pro Lys Arg Gly Glu Val Val Val Phe Ile Pro  
 85 90 95  
 Pro His Glu Lys Lys Ser Tyr Tyr Val Lys Arg Asn Phe Ala Ile Gly  
 100 105 110  
 Gly Asp Glu Val Leu Phe Thr Asn Glu Gly Phe Tyr Leu His Pro Phe  
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 Glu Ser Asp Thr Asp Lys Asn Tyr Ile Ala Lys His Tyr Pro Asn Ala  
 130 135 140  
 Met Thr Lys Glu Phe Met Gly Lys Ile Phe Val Leu Asn Pro Tyr Lys  
 145 150 155 160  
 Asn Glu His Pro Gly Ile His Tyr Gln Lys Asp Asn Glu Thr Phe His  
 165 170 175  
 Leu Met Glu Gln Leu Ala Thr Gln Gly Ala Glu Ala Asn Ile Ser Met  
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 Gln Leu Ile Gln Met Glu Gly Glu Lys Val Phe Tyr Lys Lys Ile Asn  
 195 200 205  
 Asp Asp Glu Phe Phe Met Ile Gly Asp Asn Arg Asp Asn Ser Ser Asp  
 210 215 220  
 Ser Arg Phe Trp Gly Ser Val Ala Tyr Lys Asn Ile Val Gly Ser Pro  
 225 230 235 240  
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 Met Gly

gca gtg gtt gtt tta ttt tta acg ctg gtt tta ttg ttt tta gtt tta 165  
 Ala Val Val Val Leu Phe Leu Thr Leu Val Leu Leu Phe Leu Val Leu  
                   5                                  10                                  15

agg gat ttt ggt tta gca agc ccc aaa caa aag att tta gct ttt tta 213  
 Arg Asp Phe Gly Leu Ala Ser Pro Lys Gln Lys Ile Leu Ala Phe Leu  
           20                                  25                                  30

atc gta ggg att ata gga gcg agc atc agc gtt tat act tac aag caa 261  
 Ile Val Gly Ile Ile Gly Ala Ser Ile Ser Val Tyr Thr Tyr Lys Gln  
           35                                  40                                  45                                  50

aac caa caa aac caa caa gag atc gct ttg caa aga gcg ttt tta agg 309  
 Asn Gln Gln Asn Gln Gln Glu Ile Ala Leu Gln Arg Ala Phe Leu Arg  
                                   55                                  60                                  65

ggg gaa acc ttg ttg tgt aaa ggc att aaa gtc aat aac caa acc ttt 357  
 Gly Glu Thr Leu Leu Cys Lys Gly Ile Lys Val Asn Asn Gln Thr Phe  
                   70                                  75                                  80

aat tta gtg agc gga act tta agc ttt tta ggc aaa aaa caa acc cct 405  
 Asn Leu Val Ser Gly Thr Leu Ser Phe Leu Gly Lys Lys Gln Thr Pro  
                   85                                  90                                  95

atg aaa gac gtt ctt gtg gat ttg gat tct tgt cag acg ctc caa aaa 453  
 Met Lys Asp Val Leu Val Asp Leu Asp Ser Cys Gln Thr Leu Gln Lys  
           100                                  105                                  110

gat ccc tta atc caa ccc taatgatgaa taataataat accccaccca 501  
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 Phe Leu Ile Val Gly Ile Ile Gly Ala Ser Ile Ser Val Tyr Thr Tyr  
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 Lys Gln Asn Gln Gln Asn Gln Gln Glu Ile Ala Leu Gln Arg Ala Phe  
           50                                  55                                  60  
 Leu Arg Gly Glu Thr Leu Leu Cys Lys Gly Ile Lys Val Asn Asn Gln  
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 Thr Phe Asn Leu Val Ser Gly Thr Leu Ser Phe Leu Gly Lys Lys Gln  
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 Thr Pro Met Lys Asp Val Leu Val Asp Leu Asp Ser Cys Gln Thr Leu  
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 aaaccaacga aacc atg aaa aaa gct ctc tta cta act ctc tct ctc tcg 170  
                   Met Lys Lys Ala Leu Leu Leu Thr Leu Ser Leu Ser  
                   1                  5                  10

ttc tgg ctc cac gct gaa agg aat gga ttt tat tta ggt tta aat ttt 218  
 Phe Trp Leu His Ala Glu Arg Asn Gly Phe Tyr Leu Gly Leu Asn Phe  
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cta gaa gga agc tat att aaa gga caa ggt agc atc ggc aaa aaa gct 266  
 Leu Glu Gly Ser Tyr Ile Lys Gly Gln Gly Ser Ile Gly Lys Lys Ala  
                   30                  35                  40

tca gca gaa aac gcc tta aat gaa gcg atc aat aac gca aaa aat tca 314  
 Ser Ala Glu Asn Ala Leu Asn Glu Ala Ile Asn Asn Ala Lys Asn Ser  
                   45                  50                  55                  60

tta ttc cct aac aca aaa gcc ata aga gat gca caa aac gcc tta aat 362  
 Leu Phe Pro Asn Thr Lys Ala Ile Arg Asp Ala Gln Asn Ala Leu Asn  
                   65                  70                  75

gca gtg aaa gat tca aac aaa atc gct agc cga ttc gca gga aat ggt 410  
 Ala Val Lys Asp Ser Asn Lys Ile Ala Ser Arg Phe Ala Gly Asn Gly  
                   80                  85                  90

gga tcg ggc ggt ctt ttt aat gag ctc agc ttt ggg tat aaa tat ttt 458  
 Gly Ser Gly Gly Leu Phe Asn Glu Leu Ser Phe Gly Tyr Lys Tyr Phe  
                   95                  100                  105

ttg ggt aaa aaa agg att ata ggg ttt agg cac tct ctt ttt ttc ggt 506  
 Leu Gly Lys Lys Arg Ile Ile Gly Phe Arg His Ser Leu Phe Phe Gly  
                   110                  115                  120

tac caa ctt ggt ggc gtt ggt tct gtt cct ggt agc ggt tta atc gtt 554  
 Tyr Gln Leu Gly Gly Val Gly Ser Val Pro Gly Ser Gly Leu Ile Val  
                   125                  130                  135                  140

ttt tta ccc tat ggt ttc aat acg gat ttg ctc att aat tgg act aac 602  
 Phe Leu Pro Tyr Gly Phe Asn Thr Asp Leu Leu Ile Asn Trp Thr Asn  
                   145                  150                  155

gat aag cga gcg tcc caa aaa tat gtt gaa cga agg gta aaa ggg ctc 650  
 Asp Lys Arg Ala Ser Gln Lys Tyr Val Glu Arg Arg Val Lys Gly Leu  
                   160                  165                  170

tct ata ttt tac aaa gat atg acc ggc aga acg cta gac gct aat aca 698  
 Ser Ile Phe Tyr Lys Asp Met Thr Gly Arg Thr Leu Asp Ala Asn Thr  
                   175                  180                  185

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Leu Lys Lys Ala Ser Arg His Val Phe Arg Lys Ser Ser Gly Leu Val	
190 195 200	
att ggc atg gaa cta ggg ggt agc act tgg ttt gca agt aac aat ctc	794
Ile Gly Met Glu Leu Gly Gly Ser Thr Trp Phe Ala Ser Asn Asn Leu	
205 210 215 220	
acc cct ttc aat caa gtc aag agt cgc acg att ttt cag ttg caa gga	842
Thr Pro Phe Asn Gln Val Lys Ser Arg Thr Ile Phe Gln Leu Gln Gly	
225 230 235	
aaa ttt ggc gtt cgt tgg aat aat gat gaa tac gat att gat cgc tat	890
Lys Phe Gly Val Arg Trp Asn Asn Asp Glu Tyr Asp Ile Asp Arg Tyr	
240 245 250	
ggc gat gaa atc tat ctt gga ggt tct agt gtt gaa tta ggg gtt aaa	938
Gly Asp Glu Ile Tyr Leu Gly Gly Ser Ser Val Glu Leu Gly Val Lys	
255 260 265	
gtg cca gcg ttt aaa gtc aat tac tat agc gat gat tat ggg gat aaa	986
Val Pro Ala Phe Lys Val Asn Tyr Tyr Ser Asp Asp Tyr Gly Asp Lys	
270 275 280	
ttg gat tat aaa aga gtg gtg agc gtt tat ctt aac tat aca tat aac	1034
Leu Asp Tyr Lys Arg Val Val Ser Val Tyr Leu Asn Tyr Thr Tyr Asn	
285 290 295 300	
ttt aaa aac aaa cat taaaacacgc tttttaccgc tcttttagttg gttttttaaa	1089
Phe Lys Asn Lys His	
305	
aaaccttatt ttttattagc ttgaaactct tcaaagcctt tttttctcaa ttggcatgcc	1149
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Tyr Ile Lys Gly Gln Gly Ser Ile Gly Lys Lys Ala Ser Ala Glu Asn	
35 40 45	
Ala Leu Asn Glu Ala Ile Asn Asn Ala Lys Asn Ser Leu Phe Pro Asn	
50 55 60	
Thr Lys Ala Ile Arg Asp Ala Gln Asn Ala Leu Asn Ala Val Lys Asp	
65 70 75 80	
Ser Asn Lys Ile Ala Ser Arg Phe Ala Gly Asn Gly Gly Ser Gly Gly	
85 90 95	
Leu Phe Asn Glu Leu Ser Phe Gly Tyr Lys Tyr Phe Leu Gly Lys Lys	
100 105 110	
Arg Ile Ile Gly Phe Arg His Ser Leu Phe Phe Gly Tyr Gln Leu Gly	
115 120 125	

Gly Val Gly Ser Val Pro Gly Ser Gly Leu Ile Val Phe Leu Pro Tyr  
 130 135 140  
 Gly Phe Asn Thr Asp Leu Leu Ile Asn Trp Thr Asn Asp Lys Arg Ala  
 145 150 155 160  
 Ser Gln Lys Tyr Val Gly Arg Arg Val Lys Gly Leu Ser Ile Phe Tyr  
 165 170 175  
 Lys Asp Met Thr Gly Arg Thr Leu Asp Ala Asn Thr Leu Lys Lys Ala  
 180 185 190  
 Ser Arg His Val Phe Arg Lys Ser Ser Gly Leu Val Ile Gly Met Glu  
 195 200 205  
 Leu Gly Gly Ser Thr Trp Phe Ala Ser Asn Asn Leu Thr Pro Phe Asn  
 210 215 220  
 Gln Val Lys Ser Arg Thr Ile Phe Gln Leu Gln Gly Lys Phe Gly Val  
 225 230 235 240  
 Arg Trp Asn Asn Asp Glu Tyr Asp Ile Asp Arg Tyr Gly Asp Glu Ile  
 245 250 255  
 Tyr Leu Gly Gly Ser Ser Val Glu Leu Gly Val Lys Val Pro Ala Phe  
 260 265 270  
 Lys Val Asn Tyr Tyr Ser Asp Asp Tyr Gly Asp Lys Leu Asp Tyr Lys  
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 tccaatcaaa cgcctaaaga a atg aaa gtc aag tcc att tct tat gtc ggg 171  
 Met Lys Val Lys Ser Ile Ser Tyr Val Gly  
 1 5 10  
 ctt tot tac atg tot gac atg ctc gct aat gaa att gta aag att cgt 219  
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 15 20 25  
 gtg ggc gat att gtg gat tct aaa aaa ata gac acc gct gtt ttg gct 267  
 Val Gly Asp Ile Val Asp Ser Lys Lys Ile Asp Thr Ala Val Leu Ala  
 30 35 40  
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 Leu Phe Asn Gln Gly Tyr Phe Lys Asp Val Tyr Ala Thr Phe Glu Gly  
 45 50 55  
 ggc ata tta gag ttt cat ttt gat gaa aaa gcc agg att gcc ggg gta 363  
 Gly Ile Leu Glu Phe His Phe Asp Glu Lys Ala Arg Ile Ala Gly Val  
 60 65 70  
 gaa atc aag ggt tat ggg act gaa aag gaa aaa gac ggc tta aaa tcc 411

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Gln	Met	Gly	Ile	Lys	Lys	Gly	Asp	Thr	Phe	Asp	Glu	Gln	Lys	Leu	Glu		
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cat	gct	aaa	acg	gct	tta	aaa	acc	gct	tta	gag	ggg	cag	ggc	tat	tat	507	
His	Ala	Lys	Thr	Ala	Leu	Lys	Thr	Ala	Leu	Glu	Gly	Gln	Gly	Tyr	Tyr		
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Gly	Ser	Val	Val	Glu	Val	Arg	Thr	Glu	Lys	Val	Ser	Glu	Gly	Ala	Leu		
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Leu	Ile	Val	Phe	Asp	Val	Asn	Arg	Gly	Asp	Ser	Ile	Tyr	Ile	Lys	Gln		
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Ser	Ile	Tyr	Glu	Gly	Ser	Ala	Lys	Leu	Lys	Arg	Arg	Met	Ile	Glu	Ser		
155					160					165					170		
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Leu	Ser	Ala	Asn	Lys	Gln	Arg	Asp	Phe	Met	Gly	Trp	Met	Trp	Gly	Leu		
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Asn	Asp	Gly	Lys	Leu	Arg	Leu	Asp	Gln	Leu	Glu	Tyr	Asp	Ser	Met	Arg		
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Ile	Gln	Asp	Val	Tyr	Met	Arg	Arg	Gly	Tyr	Leu	Asp	Ala	His	Ile	Ser		
		205				210						215					
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Ser	Pro	Phe	Leu	Lys	Thr	Asp	Phe	Ser	Thr	His	Asp	Ala	Lys	Leu	His		
	220					225					230						
tat	aaa	gtc	aaa	gag	ggg	atc	caa	tac	agg	att	tca	gac	att	tta	ata	891	
Tyr	Lys	Val	Lys	Glu	Gly	Ile	Gln	Tyr	Arg	Ile	Ser	Asp	Ile	Leu	Ile		
235				240				245						250			
gag	att	gac	aac	ccg	gta	gtc	ccc	tta	aaa	acc	tta	gaa	aaa	gcg	ctt	939	
Glu	Ile	Asp	Asn	Pro	Val	Val	Pro	Leu	Lys	Thr	Leu	Glu	Lys	Ala	Leu		
			255					260						265			
aaa	gtg	aaa	agg	aaa	gat	gtc	ttt	aat	att	gag	cat	tta	aga	gcg	gat	987	
Lys	Val	Lys	Arg	Lys	Asp	Val	Phe	Asn	Ile	Glu	His	Leu	Arg	Ala	Asp		
			270					275					280				
gcg	caa	att	tta	aaa	acc	gaa	atc	gcc	gat	aag	ggg	tat	gcg	ttt	gcg	1035	
Ala	Gln	Ile	Leu	Lys	Thr	Glu	Ile	Ala	Asp	Lys	Gly	Tyr	Ala	Phe	Ala		
		285				290						295					
gtg	gtg	aag	cca	gac	ttg	gat	aaa	gat	gaa	aaa	aac	ggg	ctt	gtg	aaa	1083	
Val	Val	Lys	Pro	Asp	Leu	Asp	Lys	Asp	Glu	Lys	Asn	Gly	Leu	Val	Lys		
	300					305					310						

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tcc gaa aat tct tta agg cgt tta gga ttc ttc tct aaa gtc aaa att Ser Glu Asn Ser Leu Arg Arg Leu Gly Phe Phe Ser Lys Val Lys Ile 365 370 375	1275
gaa gaa aaa agg gtt aat agc tca ctc atg gat tta tta gtg agc gta Glu Glu Lys Arg Val Asn Ser Ser Leu Met Asp Leu Leu Val Ser Val 380 385 390	1323
gaa gag ggg cgt act ggg cag ttg caa ttt ggg tta ggc tat ggc tct Glu Glu Gly Arg Thr Gly Gln Leu Gln Phe Gly Leu Gly Tyr Gly Ser 395 400 405 410	1371
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ggg aga tct tat ccg ggc atg cca aaa gga gcg ggg cgt atg ttt gcc Gly Arg Ser Tyr Pro Gly Met Pro Lys Gly Ala Gly Arg Met Phe Ala 445 450 455	1515
ggg aat ttg agc ttg act aat cca agg att ttt gac agc tgg tat agc Gly Asn Leu Ser Leu Thr Asn Pro Arg Ile Phe Asp Ser Trp Tyr Ser 460 465 470	1563
tct acg atc aac ctt tat gcg gat tac agg ata agc tac caa tac atc Ser Thr Ile Asn Leu Tyr Ala Asp Tyr Arg Ile Ser Tyr Gln Tyr Ile 475 480 485 490	1611
caa caa ggc ggg ggc ttt ggg gtg aat gtc ggg cgc atg ctg ggt aat Gln Gln Gly Gly Gly Phe Gly Val Asn Val Gly Arg Met Leu Gly Asn 495 500 505	1659
aga acc cat gtg agc tta ggg tat aac ttg aat gtt acc aaa ctc ctt Arg Thr His Val Ser Leu Gly Tyr Asn Leu Asn Val Thr Lys Leu Leu 510 515 520	1707
ggg ttc agc agc cct tta tac aac cgc tac tat tcc tct gtt aat gaa Gly Phe Ser Ser Pro Leu Tyr Asn Arg Tyr Tyr Ser Ser Val Asn Glu 525 530 535	1755
gtg gtt tct cca agg caa tgt tct acc ccc gca tgc gtg att atc aat Val Val Ser Pro Arg Gln Cys Ser Thr Pro Ala Ser Val Ile Ile Asn 540 545 550	1803

cgc tta tca ggc ggt aaa acc ccc tta caa cct gaa agc tgt tct agt	1851
Arg Leu Ser Gly Gly Lys Thr Pro Leu Gln Pro Glu Ser Cys Ser Ser	
555 560 565 570	
cct gga gcg atc acc act tca cca gaa ata aga ggt att tgg gat agg	1899
Pro Gly Ala Ile Thr Thr Ser Pro Glu Ile Arg Gly Ile Trp Asp Arg	
575 580 585	
gat tac cat acg cct atc acc agc tct ttc acc ctt gat gtg agc tat	1947
Asp Tyr His Thr Pro Ile Thr Ser Ser Phe Thr Leu Asp Val Ser Tyr	
590 595 600	
gac aac acc gat gat tat tac ttc cct aga aat ggg gtt atc ttt agt	1995
Asp Asn Thr Asp Asp Tyr Tyr Phe Pro Arg Asn Gly Val Ile Phe Ser	
605 610 615	
tcc tat gcg acg atg tct ggc ttg cca agc tct ggc acg ctc aat tct	2043
Ser Tyr Ala Thr Met Ser Gly Leu Pro Ser Ser Gly Thr Leu Asn Ser	
620 625 630	
tgg aac ggg tta ggc ggg aat gtc cgt aac acc aaa gtt tat ggt aaa	2091
Trp Asn Gly Leu Gly Gly Asn Val Arg Asn Thr Lys Val Tyr Gly Lys	
635 640 645 650	
ttc gcc gct tac cac cat ttg caa aaa tat tta ttg ata gat ttg atc	2139
Phe Ala Ala Tyr His His Leu Gln Lys Tyr Leu Leu Ile Asp Leu Ile	
655 660 665	
gct cgc ttt aaa acg caa gga ggt tat atc ttt agg tat aac acc gat	2187
Ala Arg Phe Lys Thr Gln Gly Gly Tyr Ile Phe Arg Tyr Asn Thr Asp	
670 675 680	
gat tac ttg ccc tta aac tcc acc ttc tac atg ggg ggc gta acc acg	2235
Asp Tyr Leu Pro Leu Asn Ser Thr Phe Tyr Met Gly Gly Val Thr Thr	
685 690 695	
gtg aga ggc ttt agg aac gga tcg gtt act cct aaa gat gag ttt ggc	2283
Val Arg Gly Phe Arg Asn Gly Ser Val Thr Pro Lys Asp Glu Phe Gly	
700 705 710	
ttg tgg ctt gga ggc gat ggg att ttt acc gct tct act gaa ttg agc	2331
Leu Trp Leu Gly Gly Asp Gly Ile Phe Thr Ala Ser Thr Glu Leu Ser	
715 720 725 730	
tat ggg gtg cta aag gcg gct aaa atg cgc tta gcg tgg ttt ttt gac	2379
Tyr Gly Val Leu Lys Ala Ala Lys Met Arg Leu Ala Trp Phe Phe Asp	
735 740 745	
ttt ggt ttc tta acc ttt aaa acc cca act aga ggg agt ttt ttc tat	2427
Phe Gly Phe Leu Thr Phe Lys Thr Pro Thr Arg Gly Ser Phe Phe Tyr	
750 755 760	
aac gct cct gtt acg aca gcg aat ttt aaa gat tat ggc gtt ata ggg	2475
Asn Ala Pro Val Thr Thr Ala Asn Phe Lys Asp Tyr Gly Val Ile Gly	
765 770 775	
gct ggg ttt gaa aga gcg act tgg agg gct tcc aca ggc ttg cag att	2523
Ala Gly Phe Glu Arg Ala Thr Trp Arg Ala Ser Thr Gly Leu Gln Ile	

780	785	790	
gaa tgg att tcg ccc atg ggg cct ttg gtg ttg att ttc cct ata gcg			2571
Glu Trp Ile Ser Pro Met Gly Pro Leu Val Leu Ile Phe Pro Ile Ala			
795	800	805	810
ttt ttc aac caa tgg ggc gat ggc aat ggc aag aaa tgt aaa ggg cta			2619
Phe Phe Asn Gln Trp Gly Asp Gly Asn Gly Lys Lys Cys Lys Gly Leu			
	815	820	825
tgc ttc aac cct aac atg gac gat tac acg caa cac ttt gaa ttt tct			2667
Cys Phe Asn Pro Asn Met Asp Asp Tyr Thr Gln His Phe Glu Phe Ser			
	830	835	840
atg gga aca agg ttt taaaatgcgc atcaacagag aagaaatttt ggatttaatg			2722
Met Gly Thr Arg Phe			
	845		
aaaaacgcgc ccttgaaaga attggggcaa agggctttga ggggtgaagca acgcttgcac			2782
cctgaaaact tgacgacttt tattgtggat aggaatatca attacaccaa tatttgtttt			2842
gtggattgca agttttgcgc gttcaaacgc accttaaaag aaaaagacgc ctatgtgttg			2902
agctatgaag aaattgatca aaagattgaa gaattgctcg ctattggcgg cacgcagatc			2962
ctttttcaag ggggggtgca cccgcagcta aagattgatt attatgagaa			3012
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<213> Helicobacter pylori			
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Met Leu Ala Asn Glu Ile Val Lys Ile Arg Val Gly Asp Ile Val Asp			
	20	25	30
Ser Lys Lys Ile Asp Thr Ala Val Leu Ala Leu Phe Asn Gln Gly Tyr			
	35	40	45
Phe Lys Asp Val Tyr Ala Thr Phe Glu Gly Gly Ile Leu Glu Phe His			
	50	55	60
Phe Asp Glu Lys Ala Arg Ile Ala Gly Val Glu Ile Lys Gly Tyr Gly			
65	70	75	80
Thr Glu Lys Glu Lys Asp Gly Leu Lys Ser Gln Met Gly Ile Lys Lys			
	85	90	95
Gly Asp Thr Phe Asp Glu Gln Lys Leu Glu His Ala Lys Thr Ala Leu			
	100	105	110
Lys Thr Ala Leu Glu Gly Gln Gly Tyr Tyr Gly Ser Val Val Glu Val			
	115	120	125
Arg Thr Glu Lys Val Ser Glu Gly Ala Leu Leu Ile Val Phe Asp Val			
	130	135	140
Asn Arg Gly Asp Ser Ile Tyr Ile Lys Gln Ser Ile Tyr Glu Gly Ser			
145	150	155	160
Ala Lys Leu Lys Arg Arg Met Ile Glu Ser Leu Ser Ala Asn Lys Gln			
	165	170	175
Arg Asp Phe Met Gly Trp Met Trp Gly Leu Asn Asp Gly Lys Leu Arg			
	180	185	190
Leu Asp Gln Leu Glu Tyr Asp Ser Met Arg Ile Gln Asp Val Tyr Met			
	195	200	205
Arg Arg Gly Tyr Leu Asp Ala His Ile Ser Ser Pro Phe Leu Lys Thr			
	210	215	220
Asp Phe Ser Thr His Asp Ala Lys Leu His Tyr Lys Val Lys Glu Gly			

225	Ile	Gln	Tyr	Arg	Ile	Ser	Asp	Ile	Leu	Ile	Glu	Ile	Asp	Asn	Pro	Val
					245					250					255	
Val	Pro	Leu	Lys	Thr	Leu	Glu	Lys	Ala	Leu	Lys	Val	Lys	Arg	Lys	Asp	
			260					265						270		
Val	Phe	Asn	Ile	Glu	His	Leu	Arg	Ala	Asp	Ala	Gln	Ile	Leu	Lys	Thr	
		275					280					285				
Glu	Ile	Ala	Asp	Lys	Gly	Tyr	Ala	Phe	Ala	Val	Val	Lys	Pro	Asp	Leu	
	290					295				300						
Asp	Lys	Asp	Glu	Lys	Asn	Gly	Leu	Val	Lys	Val	Ile	Tyr	Arg	Ile	Glu	
305					310					315					320	
Val	Gly	Asp	Met	Val	Tyr	Ile	Asn	Asp	Val	Ile	Ile	Ser	Gly	Asn	Gln	
				325					330					335		
Arg	Thr	Ser	Asp	Arg	Ile	Ile	Arg	Arg	Glu	Leu	Leu	Leu	Gly	Pro	Lys	
			340					345						350		
Asp	Lys	Tyr	Asn	Leu	Thr	Lys	Leu	Arg	Asn	Ser	Glu	Asn	Ser	Leu	Arg	
		355					360					365				
Arg	Leu	Gly	Phe	Phe	Ser	Lys	Val	Lys	Ile	Glu	Glu	Lys	Arg	Val	Asn	
	370					375					380					
Ser	Ser	Leu	Met	Asp	Leu	Leu	Val	Ser	Val	Glu	Glu	Gly	Arg	Thr	Gly	
385					390					395					400	
Gln	Leu	Gln	Phe	Gly	Leu	Gly	Tyr	Gly	Ser	Tyr	Gly	Gly	Leu	Met	Leu	
				405					410					415		
Asn	Gly	Ser	Val	Ser	Glu	Arg	Asn	Leu	Phe	Gly	Thr	Gly	Gln	Ser	Met	
			420					425					430			
Ser	Leu	Tyr	Ala	Asn	Ile	Ala	Thr	Gly	Gly	Gly	Arg	Ser	Tyr	Pro	Gly	
		435				440						445				
Met	Pro	Lys	Gly	Ala	Gly	Arg	Met	Phe	Ala	Gly	Asn	Leu	Ser	Leu	Thr	
	450					455					460					
Asn	Pro	Arg	Ile	Phe	Asp	Ser	Trp	Tyr	Ser	Ser	Thr	Ile	Asn	Leu	Tyr	
465					470					475					480	
Ala	Asp	Tyr	Arg	Ile	Ser	Tyr	Gln	Tyr	Ile	Gln	Gln	Gly	Gly	Gly	Phe	
				485					490					495		
Gly	Val	Asn	Val	Gly	Arg	Met	Leu	Gly	Asn	Arg	Thr	His	Val	Ser	Leu	
		500						505					510			
Gly	Tyr	Asn	Leu	Asn	Val	Thr	Lys	Leu	Leu	Gly	Phe	Ser	Ser	Pro	Leu	
		515					520					525				
Tyr	Asn	Arg	Tyr	Tyr	Ser	Ser	Val	Asn	Glu	Val	Val	Ser	Pro	Arg	Gln	
	530				535						540					
Cys	Ser	Thr	Pro	Ala	Ser	Val	Ile	Ile	Asn	Arg	Leu	Ser	Gly	Gly	Lys	
545					550					555					560	
Thr	Pro	Leu	Gln	Pro	Glu	Ser	Cys	Ser	Ser	Pro	Gly	Ala	Ile	Thr	Thr	
				565					570					575		
Ser	Pro	Glu	Ile	Arg	Gly	Ile	Trp	Asp	Arg	Asp	Tyr	His	Thr	Pro	Ile	
			580					585					590			
Thr	Ser	Ser	Phe	Thr	Leu	Asp	Val	Ser	Tyr	Asp	Asn	Thr	Asp	Asp	Tyr	
		595					600					605				
Tyr	Phe	Pro	Arg	Asn	Gly	Val	Ile	Phe	Ser	Ser	Tyr	Ala	Thr	Met	Ser	
	610					615						620				
Gly	Leu	Pro	Ser	Ser	Gly	Thr	Leu	Asn	Ser	Trp	Asn	Gly	Leu	Gly	Gly	
625					630					635					640	
Asn	Val	Arg	Asn	Thr	Lys	Val	Tyr	Gly	Lys	Phe	Ala	Ala	Tyr	His	His	
				645					650					655		
Leu	Gln	Lys	Tyr	Leu	Leu	Ile	Asp	Leu	Ile	Ala	Arg	Phe	Lys	Thr	Gln	
			660					665						670		
Gly	Gly	Tyr	Ile	Phe	Arg	Tyr	Asn	Thr	Asp	Asp	Tyr	Leu	Pro	Leu	Asn	
		675					680					685				
Ser	Thr	Phe	Tyr	Met	Gly	Gly	Val	Thr	Thr	Val	Arg	Gly	Phe	Arg	Asn	
	690					695					700					



Gly	Ser	Val	Thr	Pro	Lys	Asp	Glu	Phe	Gly	Leu	Trp	Leu	Gly	Gly	Asp
705					710					715					720
Gly	Ile	Phe	Thr	Ala	Ser	Thr	Glu	Leu	Ser	Tyr	Gly	Val	Leu	Lys	Ala
				725					730					735	
Ala	Lys	Met	Arg	Leu	Ala	Trp	Phe	Phe	Asp	Phe	Gly	Phe	Leu	Thr	Phe
			740					745					750		
Lys	Thr	Pro	Thr	Arg	Gly	Ser	Phe	Phe	Tyr	Asn	Ala	Pro	Val	Thr	Thr
		755					760					765			
Ala	Asn	Phe	Lys	Asp	Tyr	Gly	Val	Ile	Gly	Ala	Gly	Phe	Glu	Arg	Ala
	770					775					780				
Thr	Trp	Arg	Ala	Ser	Thr	Gly	Leu	Gln	Ile	Glu	Trp	Ile	Ser	Pro	Met
785					790					795					800
Gly	Pro	Leu	Val	Leu	Ile	Phe	Pro	Ile	Ala	Phe	Phe	Asn	Gln	Trp	Gly
			805						810					815	
Asp	Gly	Asn	Gly	Lys	Lys	Cys	Lys	Gly	Leu	Cys	Phe	Asn	Pro	Asn	Met
		820						825				830			
Asp	Asp	Tyr	Thr	Gln	His	Phe	Glu	Phe	Ser	Met	Gly	Thr	Arg	Phe	
		835					840					845			

<210> 9  
 <211> 1032  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (149)...(913)

<400> 9  
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 tagggggggtt tggttattgg tgtttgatta gaatagggtt gtttttaatt ttcttttaag 120  
 aggagttttt acttttttaa ggggtttt atg gat att tat gcg tta tat ata 172  
 Met Asp Ile Tyr Ala Leu Tyr Ile  
 1 5

gcg ata ggg ctt ttt act ggc att cta tca ggg att ttt ggc att ggt 220  
 Ala Ile Gly Leu Phe Thr Gly Ile Leu Ser Gly Ile Phe Gly Ile Gly  
 10 15 20

ggg ggg ttg atc att gtc cct atc atg ctc gca acc ggg cat tct ttt 268  
 Gly Gly Leu Ile Ile Val Pro Ile Met Leu Ala Thr Gly His Ser Phe  
 25 30 35 40

gaa gaa tcc att ggg att tcc att ttg caa atg gcg ctt tca tcg ttc 316  
 Glu Glu Ser Ile Gly Ile Ser Ile Leu Gln Met Ala Leu Ser Ser Phe  
 45 50 55

gtg ggc tct gtt ttg aat ttc aaa aaa aaa tcg ctt gat ttt tct tta 364  
 Val Gly Ser Val Leu Asn Phe Lys Lys Lys Ser Leu Asp Phe Ser Leu  
 60 65 70

ggc ttg ttg ata ggg gca ggg ggg ctg ata ggg gcg agt ttt agc gga 412  
 Gly Leu Leu Ile Gly Ala Gly Gly Leu Ile Gly Ala Ser Phe Ser Gly  
 75 80 85

ttt gtt tta aaa atc gtt tcc agt aaa att tta atg gtt att ttc gcg 460  
 Phe Val Leu Lys Ile Val Ser Ser Lys Ile Leu Met Val Ile Phe Ala  
 90 95 100

ctt tta gtc gtg tat tct atg atc caa ttt gtt ttg aaa ccc aaa aaa 508  
 Leu Leu Val Val Tyr Ser Met Ile Gln Phe Val Leu Lys Pro Lys Lys  
 105 110 115 120  
 aaa gat ttg ata gcg gat act aaa cgc tat cat ctg caa ggt ttg aaa 556  
 Lys Asp Leu Ile Ala Asp Thr Lys Arg Tyr His Leu Gln Gly Leu Lys  
 125 130 135  
 tta ttt tta att ggc acg ctc aca ggg ttt ttt gct atc act tta ggg 604  
 Leu Phe Leu Ile Gly Thr Leu Thr Gly Phe Phe Ala Ile Thr Leu Gly  
 140 145 150  
 att ggt ggg ggg atg ctc atg gtg cct ttg atg cat tat ttt tta ggg 652  
 Ile Gly Gly Gly Met Leu Met Val Pro Leu Met His Tyr Phe Leu Gly  
 155 160 165  
 tat gat tct aaa aaa tgc gtg gct cta ggg tta ttt ttc atc ttg ttt 700  
 Tyr Asp Ser Lys Lys Cys Val Ala Leu Gly Leu Phe Phe Ile Leu Phe  
 170 175 180  
 tct tct att tca gga gct ttt tct tta atg tat cac cac atc atc aat 748  
 Ser Ser Ile Ser Gly Ala Phe Ser Leu Met Tyr His His Ile Ile Asn  
 185 190 195 200  
 aaa gaa gtg ctc tta gca ggg gcg att gtg gga tta gga tct gtt atg 796  
 Lys Glu Val Leu Leu Ala Gly Ala Ile Val Gly Leu Gly Ser Val Met  
 205 210 215  
 ggc gtg agc att ggg att aaa tgg atc atg ggg ctt ttg aat gaa aaa 844  
 Gly Val Ser Ile Gly Ile Lys Trp Ile Met Gly Leu Leu Asn Glu Lys  
 220 225 230  
 atg cat aaa gct ttg att tta ggg gtg tat ggt ttg tcg cta ttg att 892  
 Met His Lys Ala Leu Ile Leu Gly Val Tyr Gly Leu Ser Leu Leu Ile  
 235 240 245  
 gtt tta tac aaa ctc ttt ttt taattgatgg ttttatacca ctactatttt 943  
 Val Leu Tyr Lys Leu Phe Phe  
 250 255  
 aagaccoccta agagtttccc tttagagtat ttgcatttgt gcgctaata gagccattta 1003  
 ttgagattgg attttgatgc ggccaattt 1032

<210> 10  
 <211> 255  
 <212> PRT  
 <213> Helicobacter pylori

<400> 10  
 Met Asp Ile Tyr Ala Leu Tyr Ile Ala Ile Gly Leu Phe Thr Gly Ile  
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 Leu Ser Gly Ile Phe Gly Ile Gly Gly Leu Ile Ile Val Pro Ile  
 20 25 30  
 Met Leu Ala Thr Gly His Ser Phe Glu Glu Ser Ile Gly Ile Ser Ile  
 35 40 45  
 Leu Gln Met Ala Leu Ser Ser Phe Val Gly Ser Val Leu Asn Phe Lys  
 50 55 60  
 Lys Lys Ser Leu Asp Phe Ser Leu Gly Leu Leu Ile Gly Ala Gly Gly

65	70	75	80
Leu Ile Gly Ala Ser Phe Ser Gly Phe Val Leu Lys Ile Val Ser Ser			
	85	90	95
Lys Ile Leu Met Val Ile Phe Ala Leu Leu Val Val Tyr Ser Met Ile			
	100	105	110
Gln Phe Val Leu Lys Pro Lys Lys Asp Leu Ile Ala Asp Thr Lys			
	115	120	125
Arg Tyr His Leu Gln Gly Leu Lys Leu Phe Leu Ile Gly Thr Leu Thr			
	130	135	140
Gly Phe Phe Ala Ile Thr Leu Gly Ile Gly Gly Gly Met Leu Met Val			
	145	150	155
Pro Leu Met His Tyr Phe Leu Gly Tyr Asp Ser Lys Lys Cys Val Ala			
	165	170	175
Leu Gly Leu Phe Phe Ile Leu Phe Ser Ser Ile Ser Gly Ala Phe Ser			
	180	185	190
Leu Met Tyr His His Ile Ile Asn Lys Glu Val Leu Leu Ala Gly Ala			
	195	200	205
Ile Val Gly Leu Gly Ser Val Met Gly Val Ser Ile Gly Ile Lys Trp			
	210	215	220
Ile Met Gly Leu Leu Asn Glu Lys Met His Lys Ala Leu Ile Leu Gly			
	225	230	235
Val Tyr Gly Leu Ser Leu Leu Ile Val Leu Tyr Lys Leu Phe Phe			
	245	250	255

<210> 11  
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 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (66)...(980)

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 ccgtt atg ggt aga att gaa tca aaa aag cgt ttg aaa gcg ctt gtt ttt 110  
 Met Gly Arg Ile Glu Ser Lys Lys Arg Leu Lys Ala Leu Val Phe  
 1 5 10 15  
  
 tta gcc agc ttg ggg gtt ttg tgg ggc aat agc gct gaa aaa acg cct 158  
 Leu Ala Ser Leu Gly Val Leu Trp Gly Asn Ser Ala Glu Lys Thr Pro  
 20 25 30  
  
 ttt ttt aaa acg aaa aac cac att tat cta ggt ttt agg cta ggc aca 206  
 Phe Phe Lys Thr Lys Asn His Ile Tyr Leu Gly Phe Arg Leu Gly Thr  
 35 40 45  
  
 gga gcc aat gtg cac acg agc atg tgg caa caa gcc tat aaa gac aac 254  
 Gly Ala Asn Val His Thr Ser Met Trp Gln Gln Ala Tyr Lys Asp Asn  
 50 55 60  
  
 ccc acc tgc cct ggt agc gtg tgt tat ggc gag aaa tta gaa gcc cat 302  
 Pro Thr Cys Pro Gly Ser Val Cys Tyr Gly Glu Lys Leu Glu Ala His  
 65 70 75  
  
 tat cag ggg ggt aaa aac ctg tct tat acc ggg caa ata ggc gat gaa 350  
 Tyr Gln Gly Gly Lys Asn Leu Ser Tyr Thr Gly Gln Ile Gly Asp Glu  
 80 85 90 95

ata gct ttt gat aaa cac cat att tta ggc tta agg gtg tgg ggg gat Ile Ala Phe Asp Lys His His Ile Leu Gly Leu Arg Val Trp Gly Asp 100 105 110	398
gta gaa tac gct aaa gcg caa tta ggt caa aaa gtg ggg ggt aat acc Val Glu Tyr Ala Lys Ala Gln Leu Gly Gln Lys Val Gly Gly Asn Thr 115 120 125	446
ctt tta tcc caa gcc aat tat gac cca aac gcg att aaa acc tac gat Leu Leu Ser Gln Ala Asn Tyr Asp Pro Asn Ala Ile Lys Thr Tyr Asp 130 135 140	494
tct gct tca aac act caa ggc cct tta gtt ttg caa aaa acc cca agc Ser Ala Ser Asn Thr Gln Gly Pro Leu Val Leu Gln Lys Thr Pro Ser 145 150 155	542
cct caa aac ttc ctt ttc aat aac ggg cat ttc atg gcg ttt ggt ttg Pro Gln Asn Phe Leu Phe Asn Asn Gly His Phe Met Ala Phe Gly Leu 160 165 170 175	590
aac gtg aat gtg ttt gtt aac ctc cct ata gac acc ctt tta aaa ctc Asn Val Asn Val Phe Val Asn Leu Pro Ile Asp Thr Leu Leu Lys Leu 180 185 190	638
gct tta aaa aca gaa aaa atg ctg ttt ttt aaa ata ggc gtg ttt ggt Ala Leu Lys Thr Glu Lys Met Leu Phe Phe Lys Ile Gly Val Phe Gly 195 200 205	686
ggg ggc ggg gtg gaa tac gca ata tta tgg agt cct aac tat caa aat Gly Gly Gly Val Glu Tyr Ala Ile Leu Trp Ser Pro Asn Tyr Gln Asn 210 215 220	734
caa aac acg aaa caa ggc gat aaa ttt ttt gca gcg ggt ggg ggg ttt Gln Asn Thr Lys Gln Gly Asp Lys Phe Phe Ala Ala Gly Gly Gly Phe 225 230 235	782
ttt gtg aat ttt ggg ggt tct ttg tat ata ggc aaa cgc aac cgc ttc Phe Val Asn Phe Gly Gly Ser Leu Tyr Ile Gly Lys Arg Asn Arg Phe 240 245 250 255	830
aat gtg ggg tta aaa atc cct tac tat agc ttg agc gcg caa agt tgg Asn Val Gly Leu Lys Ile Pro Tyr Tyr Ser Leu Ser Ala Gln Ser Trp 260 265 270	878
aaa aac ttt ggc tct agc aat gtg tgg cag caa caa acg atc cga caa Lys Asn Phe Gly Ser Ser Asn Val Trp Gln Gln Gln Thr Ile Arg Gln 275 280 285	926
aac ttc agc gtt ttt agg aat aaa gaa gtt ttt gtc agc tac gcg ttc Asn Phe Ser Val Phe Arg Asn Lys Glu Val Phe Val Ser Tyr Ala Phe 290 295 300	974
ttg ttt tagtttggat tcgttctcat taaacactga tgataaaatt caaaagatgg Leu Phe 305	1030
ttttatcggtt acaaaattca acatttc	1057

<210> 12  
 <211> 305  
 <212> PRT  
 <213> Helicobacter pylori

<400> 12  
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 Ala Ser Leu Gly Val Leu Trp Gly Asn Ser Ala Glu Lys Thr Pro Phe  
 20 25 30  
 Phe Lys Thr Lys Asn His Ile Tyr Leu Gly Phe Arg Leu Gly Thr Gly  
 35 40 45  
 Ala Asn Val His Thr Ser Met Trp Gln Gln Ala Tyr Lys Asp Asn Pro  
 50 55 60  
 Thr Cys Pro Gly Ser Val Cys Tyr Gly Glu Lys Leu Glu Ala His Tyr  
 65 70 75 80  
 Gln Gly Gly Lys Asn Leu Ser Tyr Thr Gly Gln Ile Gly Asp Glu Ile  
 85 90 95  
 Ala Phe Asp Lys His His Ile Leu Gly Leu Arg Val Trp Gly Asp Val  
 100 105 110  
 Glu Tyr Ala Lys Ala Gln Leu Gly Gln Lys Val Gly Gly Asn Thr Leu  
 115 120 125  
 Leu Ser Gln Ala Asn Tyr Asp Pro Asn Ala Ile Lys Thr Tyr Asp Ser  
 130 135 140  
 Ala Ser Asn Thr Gln Gly Pro Leu Val Leu Gln Lys Thr Pro Ser Pro  
 145 150 155 160  
 Gln Asn Phe Leu Phe Asn Asn Gly His Phe Met Ala Phe Gly Leu Asn  
 165 170 175  
 Val Asn Val Phe Val Asn Leu Pro Ile Asp Thr Leu Leu Lys Leu Ala  
 180 185 190  
 Leu Lys Thr Glu Lys Met Leu Phe Phe Lys Ile Gly Val Phe Gly Gly  
 195 200 205  
 Gly Gly Val Glu Tyr Ala Ile Leu Trp Ser Pro Asn Tyr Gln Asn Gln  
 210 215 220  
 Asn Thr Lys Gln Gly Asp Lys Phe Phe Ala Ala Gly Gly Gly Phe Phe  
 225 230 235 240  
 Val Asn Phe Gly Gly Ser Leu Tyr Ile Gly Lys Arg Asn Arg Phe Asn  
 245 250 255  
 Val Gly Leu Lys Ile Pro Tyr Tyr Ser Leu Ser Ala Gln Ser Trp Lys  
 260 265 270  
 Asn Phe Gly Ser Ser Asn Val Trp Gln Gln Gln Thr Ile Arg Gln Asn  
 275 280 285  
 Phe Ser Val Phe Arg Asn Lys Glu Val Phe Val Ser Tyr Ala Phe Leu  
 290 295 300  
 Phe  
 305

<210> 13  
 <211> 624  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (77)...(535)

<400> 13  
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taaaaggggt tttata atg gaa aac aac gaa aat cat gag aaa ttg aat ggc 112  
                     Met Glu Asn Asn Glu Asn His Glu Lys Leu Asn Gly  
                     1                                    5                                    10

gtt ttg cgc aag ttt tta ggc gat gcg ttc acg ctt gat ggg aaa gaa 160  
 Val Leu Arg Lys Phe Leu Gly Asp Ala Phe Thr Leu Asp Gly Lys Glu  
                     15                                    20                                    25

gga gga ttg aat atg gaa aaa ttg cgc gaa gcc att aaa aaa gaa aaa 208  
 Gly Gly Leu Asn Met Glu Lys Leu Arg Glu Ala Ile Lys Lys Glu Lys  
                     30                                    35                                    40

cca atc atg aat att ttg ctc atg gga gct act ggg gtg ggt aaa agc 256  
 Pro Ile Met Asn Ile Leu Leu Met Gly Ala Thr Gly Val Gly Lys Ser  
                     45                                    50                                    55                                    60

tcg ctc att aac gct cta ttc ggt aag gaa gta gct aaa gca ggt gta 304  
 Ser Leu Ile Asn Ala Leu Phe Gly Lys Glu Val Ala Lys Ala Gly Val  
                                     65                                    70                                    75

gga aaa ccc atc act cag cat ctt gaa aaa tat gtt gat gaa gaa aaa 352  
 Gly Lys Pro Ile Thr Gln His Leu Glu Lys Tyr Val Asp Glu Glu Lys  
                                     80                                    85                                    90

ggc ttg att tta tgg gac act aaa ggc att gaa gat aaa gat tat gaa 400  
 Gly Leu Ile Leu Trp Asp Thr Lys Gly Ile Glu Asp Lys Asp Tyr Glu  
                                     95                                    100                                    105

aat acc ttg gaa agc att aaa aaa gaa atg gaa gat tct ttt aaa acg 448  
 Asn Thr Leu Glu Ser Ile Lys Lys Glu Met Glu Asp Ser Phe Lys Thr  
                     110                                    115                                    120

ctt gat gaa aaa gag gct att gat gtg gcg tat ctg tgc gtt aaa gag 496  
 Leu Asp Glu Lys Glu Ala Ile Asp Val Ala Tyr Leu Cys Val Lys Glu  
                     125                                    130                                    135                                    140

act tct ggt agg gtt caa gag aga gag aga gag agt tat taagctttac 545  
 Thr Ser Gly Arg Val Gln Glu Arg Glu Arg Glu Ser Tyr  
                                     145                                    150

taaaaaatgg aatatcccaa cgattttcgt tttcaccaac acacaagaaa aagccggcga 605  
 tgccttttggt aaaaaaact 624

<210> 14  
 <211> 153  
 <212> PRT  
 <213> Helicobacter pylori

<400> 14  
 Met Glu Asn Asn Glu Asn His Glu Lys Leu Asn Gly Val Leu Arg Lys  
                     1                                    5                                    10                                    15  
 Phe Leu Gly Asp Ala Phe Thr Leu Asp Gly Lys Glu Gly Gly Leu Asn  
                                     20                                    25                                    30  
 Met Glu Lys Leu Arg Glu Ala Ile Lys Lys Glu Lys Pro Ile Met Asn  
                     35                                    40                                    45  
 Ile Leu Leu Met Gly Ala Thr Gly Val Gly Lys Ser Ser Leu Ile Asn  
                     50                                    55                                    60  
 Ala Leu Phe Gly Lys Glu Val Ala Lys Ala Gly Val Gly Lys Pro Ile  
                     65                                    70                                    75                                    80

Thr Gln His Leu Glu Lys Tyr Val Asp Glu Glu Lys Gly Leu Ile Leu  
85 90 95  
Trp Asp Thr Lys Gly Ile Glu Asp Lys Asp Tyr Glu Asn Thr Leu Glu  
100 105 110  
Ser Ile Lys Lys Glu Met Glu Asp Ser Phe Lys Thr Leu Asp Glu Lys  
115 120 125  
Glu Ala Ile Asp Val Ala Tyr Leu Cys Val Lys Glu Thr Ser Gly Arg  
130 135 140  
Val Gln Glu Arg Glu Arg Glu Ser Tyr  
145 150

<210> 15  
<211> 1083  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (155)...(1033)

<400> 15  
gatgttggtta agtcgttggtt tattatgtta cactaaaagc ttaaataaaa gggcataagg 60  
gataaaggga gtgttagtag atagttttaa taggggttatt gactatatta gggtttctgt 120  
aaccaaacag tgcaatttca ggtgtcagta ttgc atg cct gct acg cca tta aat 175  
Met Pro Ala Thr Pro Leu Asn  
1 5

ttt ttt gat aat gaa gaa tta ttg cct ttg gat aat gtt tta gaa ttt 223  
Phe Phe Asp Asn Glu Glu Leu Leu Pro Leu Asp Asn Val Leu Glu Phe  
10 15 20

ctc aaa atc gcc att gat gag ggc gtt aaa aaa att aga atc acg ggt 271  
Leu Lys Ile Ala Ile Asp Glu Gly Val Lys Lys Ile Arg Ile Thr Gly  
25 30 35

ggg gag ccg cta tta cgc aaa ggc tta gat gaa ttt atc gct aaa ttg 319  
Gly Glu Pro Leu Leu Arg Lys Gly Leu Asp Glu Phe Ile Ala Lys Leu  
40 45 50 55

cac gct tac aat aaa gaa gtg gag tta gtt tta agc act aat ggt ttt 367  
His Ala Tyr Asn Lys Glu Val Glu Leu Val Leu Ser Thr Asn Gly Phe  
60 65 70

tta ctc aaa aaa atg gct aag gat tta aaa aat gcc ggg tta gcg caa 415  
Leu Leu Lys Lys Met Ala Lys Asp Leu Lys Asn Ala Gly Leu Ala Gln  
75 80 85

gtg aat gtt tca ttg gat tct tta aaa agc gat agg gtt tta aaa atc 463  
Val Asn Val Ser Leu Asp Ser Leu Lys Ser Asp Arg Val Leu Lys Ile  
90 95 100

tct caa aaa gac gct ctt aaa aac acg cta gaa ggg att gaa gag tct 511  
Ser Gln Lys Asp Ala Leu Lys Asn Thr Leu Glu Gly Ile Glu Glu Ser  
105 110 115

ttg aaa gtg ggt tta aaa ctc aaa tta aac acg gtt gtg ata aaa agc 559  
Leu Lys Val Gly Leu Lys Leu Lys Leu Asn Thr Val Val Ile Lys Ser  
120 125 130 135

gtt aat gat gat gaa atc tta gag ctt tta gaa tac gca aaa aat agg 607  
 Val Asn Asp Asp Glu Ile Leu Glu Leu Leu Glu Tyr Ala Lys Asn Arg  
 140 145 150  
 cat ata caa atc cgc tac att gaa ttt atg gaa aac acg cat gct aaa 655  
 His Ile Gln Ile Arg Tyr Ile Glu Phe Met Glu Asn Thr His Ala Lys  
 155 160 165  
 agt ttg gtt aaa ggc ttg aaa gag cga gaa att tta gat ttg atc gct 703  
 Ser Leu Val Lys Gly Leu Lys Glu Arg Glu Ile Leu Asp Leu Ile Ala  
 170 175 180  
 caa aaa tat caa atc att gag gca gaa aaa ccc aaa caa ggg tct tct 751  
 Gln Lys Tyr Gln Ile Ile Glu Ala Glu Lys Pro Lys Gln Gly Ser Ser  
 185 190 195  
 aaa atc tac acg cta gaa aat ggc tat caa ttt ggc att atc gct ccg 799  
 Lys Ile Tyr Thr Leu Glu Asn Gly Tyr Gln Phe Gly Ile Ile Ala Pro  
 200 205 210 215  
 cat agc gat gat ttt tgc caa tct tgc aat cgt atc cgt ttg gct tct 847  
 His Ser Asp Asp Phe Cys Gln Ser Cys Asn Arg Ile Arg Leu Ala Ser  
 220 225 230  
 gat ggt aag att tgc cca tgt tta tac tat caa gac gcc ata gac gct 895  
 Asp Gly Lys Ile Cys Pro Cys Leu Tyr Tyr Gln Asp Ala Ile Asp Ala  
 235 240 245  
 aaa gag gcg atc atc aat aag gat aca aaa aat ata aaa agg ctt tta 943  
 Lys Glu Ala Ile Ile Asn Lys Asp Thr Lys Asn Ile Lys Arg Leu Leu  
 250 255 260  
 aag caa tct gtc atc aat aaa cca gaa aaa aac atg tgg aat gat aaa 991  
 Lys Gln Ser Val Ile Asn Lys Pro Glu Lys Asn Met Trp Asn Asp Lys  
 265 270 275  
 aac agc gaa act ccc aca agg gcg ttt tac tac aca ggg ggg 1033  
 Asn Ser Glu Thr Pro Thr Arg Ala Phe Tyr Tyr Thr Gly Gly  
 280 285 290  
 taggggagta aaatatattat tatttttaaac ctttttatta aaaataaggc 1083

<210> 16  
 <211> 293  
 <212> PRT  
 <213> Helicobacter pylori

<400> 16  
 Met Pro Ala Thr Pro Leu Asn Phe Phe Asp Asn Glu Glu Leu Leu Pro  
 1 5 10 15  
 Leu Asp Asn Val Leu Glu Phe Leu Lys Ile Ala Ile Asp Glu Gly Val  
 20 25 30  
 Lys Lys Ile Arg Ile Thr Gly Gly Glu Pro Leu Leu Arg Lys Gly Leu  
 35 40 45  
 Asp Glu Phe Ile Ala Lys Leu His Ala Tyr Asn Lys Glu Val Glu Leu  
 50 55 60  
 Val Leu Ser Thr Asn Gly Phe Leu Leu Lys Lys Met Ala Lys Asp Leu  
 65 70 75 80



Lys Asn Ala Gly Leu Ala Gln Val Asn Val Ser Leu Asp Ser Leu Lys  
                     85                    90                    95  
 Ser Asp Arg Val Leu Lys Ile Ser Gln Lys Asp Ala Leu Lys Asn Thr  
                     100                    105                    110  
 Leu Glu Gly Ile Glu Glu Ser Leu Lys Val Gly Leu Lys Leu Lys Leu  
                     115                    120                    125  
 Asn Thr Val Val Ile Lys Ser Val Asn Asp Asp Glu Ile Leu Glu Leu  
                     130                    135                    140  
 Leu Glu Tyr Ala Lys Asn Arg His Ile Gln Ile Arg Tyr Ile Glu Phe  
 145                    150                    155                    160  
 Met Glu Asn Thr His Ala Lys Ser Leu Val Lys Gly Leu Lys Glu Arg  
                     165                    170                    175  
 Glu Ile Leu Asp Leu Ile Ala Gln Lys Tyr Gln Ile Ile Glu Ala Glu  
                     180                    185                    190  
 Lys Pro Lys Gln Gly Ser Ser Lys Ile Tyr Thr Leu Glu Asn Gly Tyr  
                     195                    200                    205  
 Gln Phe Gly Ile Ile Ala Pro His Ser Asp Asp Phe Cys Gln Ser Cys  
 210                    215                    220  
 Asn Arg Ile Arg Leu Ala Ser Asp Gly Lys Ile Cys Pro Cys Leu Tyr  
 225                    230                    235                    240  
 Tyr Gln Asp Ala Ile Asp Ala Lys Glu Ala Ile Ile Asn Lys Asp Thr  
                     245                    250                    255  
 Lys Asn Ile Lys Arg Leu Leu Lys Gln Ser Val Ile Asn Lys Pro Glu  
                     260                    265                    270  
 Lys Asn Met Trp Asn Asp Lys Asn Ser Glu Thr Pro Thr Arg Ala Phe  
                     275                    280                    285  
 Tyr Tyr Thr Gly Gly  
                     290

<210> 17  
 <211> 1181  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (121)...(1137)

<400> 17  
 acttctcaat cagcgagcta tcatgcaagg ccttatgtgg tggataccgc ttttttacga 60  
 tacgattaca aagatgtttt tgggtttaag gcggggcgct atgaagcgaa tattgatttc 120  
 atg agc gga tcg aat caa ggg tgg gaa gtg tat tat cag ccc tat aag 168  
 Met Ser Gly Ser Asn Gln Gly Trp Glu Val Tyr Tyr Gln Pro Tyr Lys  
   1                    5                    10                    15  
  
 act gaa acg caa agg tta agg ttt tgg tgg tgg agt tct ttt ggg aga 216  
 Thr Glu Thr Gln Arg Leu Arg Phe Trp Trp Trp Ser Ser Phe Gly Arg  
                     20                    25                    30  
  
 ggt tta gcg ttc aac tct tgg att tat gag ttt ttt gcg acg gtg cct 264  
 Gly Leu Ala Phe Asn Ser Trp Ile Tyr Glu Phe Phe Ala Thr Val Pro  
                     35                    40                    45  
  
 tat ttg aaa aag gga ggc aat cct aat aac agc aac gat ttc atc aat 312  
 Tyr Leu Lys Lys Gly Gly Asn Pro Asn Asn Ser Asn Asp Phe Ile Asn  
                     50                    55                    60  
  
 tat ggc tgg cat gga atc acc aca acc tat tct tat aaa ggt tta gac 360

Tyr	Gly	Trp	His	Gly	Ile	Thr	Thr	Thr	Tyr	Ser	Tyr	Lys	Gly	Leu	Asp	
65					70					75					80	
gct	caa	ttt	ttt	tat	tat	ttt	gcg	cct	aag	act	tat	aac	gct	cct	ggc	408
Ala	Gln	Phe	Phe	Tyr	Tyr	Phe	Ala	Pro	Lys	Thr	Tyr	Asn	Ala	Pro	Gly	
				85					90					95		
ttt	aag	ctg	gtc	tat	gac	acg	aat	agg	aat	ttt	caa	aat	gta	ggc	ttt	456
Phe	Lys	Leu	Val	Tyr	Asp	Thr	Asn	Arg	Asn	Phe	Gln	Asn	Val	Gly	Phe	
			100					105					110			
cgc	tct	caa	agc	atg	atc	atg	aca	acc	ttt	cct	tta	tac	tat	aga	ggg	504
Arg	Ser	Gln	Ser	Met	Ile	Met	Thr	Thr	Phe	Pro	Leu	Tyr	Tyr	Arg	Gly	
			115				120					125				
tgg	tat	aac	cca	gag	aca	aac	act	tat	agt	tta	gaa	gac	agc	acg	cct	552
Trp	Tyr	Asn	Pro	Glu	Thr	Asn	Thr	Tyr	Ser	Leu	Glu	Asp	Ser	Thr	Pro	
	130					135					140					
cat	ggc	tcg	ttg	ttg	ggg	agg	aat	ggc	gtt	act	tta	aat	atc	cgc	cag	600
His	Gly	Ser	Leu	Leu	Gly	Arg	Asn	Gly	Val	Thr	Leu	Asn	Ile	Arg	Gln	
	145				150				155						160	
gtt	ttt	tgg	tgg	gat	aat	ttc	aac	tgg	tcc	att	ggc	ttt	tat	aac	acc	648
Val	Phe	Trp	Trp	Asp	Asn	Phe	Asn	Trp	Ser	Ile	Gly	Phe	Tyr	Asn	Thr	
				165				170						175		
ttt	ggc	aat	tcg	gac	gct	ttt	tta	ggc	tct	cac	acg	atg	cca	agg	ggt	696
Phe	Gly	Asn	Ser	Asp	Ala	Phe	Leu	Gly	Ser	His	Thr	Met	Pro	Arg	Gly	
			180					185					190			
aat	aac	act	tcc	tat	atc	ggt	agt	gaa	atc	tcc	ata	acg	act	agg	cat	744
Asn	Asn	Thr	Ser	Tyr	Ile	Gly	Ser	Glu	Ile	Ser	Ile	Thr	Thr	Arg	His	
			195				200					205				
gcc	gga	atg	att	ggc	tat	gat	ttt	tgg	gat	aat	acg	gct	tat	gat	ggg	792
Ala	Gly	Met	Ile	Gly	Tyr	Asp	Phe	Trp	Asp	Asn	Thr	Ala	Tyr	Asp	Gly	
	210					215					220					
cta	gct	gat	gcg	atc	act	aac	gct	aac	act	ttc	act	ttt	tac	act	tct	840
Leu	Ala	Asp	Ala	Ile	Thr	Asn	Ala	Asn	Thr	Phe	Thr	Phe	Tyr	Thr	Ser	
	225				230					235					240	
gtt	gga	ggg	atc	cat	aag	cgt	ttt	gca	tgg	cat	gtt	ttt	ggg	cgc	gtc	888
Val	Gly	Gly	Ile	His	Lys	Arg	Phe	Ala	Trp	His	Val	Phe	Gly	Arg	Val	
				245					250					255		
tct	cat	gcg	aat	aaa	aac	gcg	tta	ggg	caa	gtg	ggg	agg	gct	aat	gaa	936
Ser	His	Ala	Asn	Lys	Asn	Ala	Leu	Gly	Gln	Val	Gly	Arg	Ala	Asn	Glu	
			260					265					270			
tat	tcc	ttg	caa	ttc	aac	gcg	agc	tat	gcg	ttc	act	gaa	tca	atc	ctt	984
Tyr	Ser	Leu	Gln	Phe	Asn	Ala	Ser	Tyr	Ala	Phe	Thr	Glu	Ser	Ile	Leu	
		275					280					285				
ctt	aac	ttt	agg	atc	act	tat	tat	ggg	gct	agg	atc	aat	aaa	ggg	tat	1032
Leu	Asn	Phe	Arg	Ile	Thr	Tyr	Tyr	Gly	Ala	Arg	Ile	Asn	Lys	Gly	Tyr	
	290					295					300					

caa gcg ggg tat ttt gga gcg ccc aaa ttc aat aac cct gat ggc gat 1080  
 Gln Ala Gly Tyr Phe Gly Ala Pro Lys Phe Asn Asn Pro Asp Gly Asp  
 305 310 315 320

ttt agc gct aat tac caa gac aga agt tac atg atg acc aac ctc acg 1128  
 Phe Ser Ala Asn Tyr Gln Asp Arg Ser Tyr Met Met Thr Asn Leu Thr  
 325 330 335

ctg aag ttt tgatttccaa tcacagcgag ttaaaaacac tccaaggcat 1177  
 Leu Lys Phe

tttt 1181

<210> 18  
 <211> 339  
 <212> PRT  
 <213> Helicobacter pylori

<400> 18  
 Met Ser Gly Ser Asn Gln Gly Trp Glu Val Tyr Tyr Gln Pro Tyr Lys  
 1 5 10 15  
 Thr Glu Thr Gln Arg Leu Arg Phe Trp Trp Trp Ser Ser Phe Gly Arg  
 20 25 30  
 Gly Leu Ala Phe Asn Ser Trp Ile Tyr Glu Phe Phe Ala Thr Val Pro  
 35 40 45  
 Tyr Leu Lys Lys Gly Gly Asn Pro Asn Asn Ser Asn Asp Phe Ile Asn  
 50 55 60  
 Tyr Gly Trp His Gly Ile Thr Thr Thr Tyr Ser Tyr Lys Gly Leu Asp  
 65 70 75 80  
 Ala Gln Phe Phe Tyr Tyr Phe Ala Pro Lys Thr Tyr Asn Ala Pro Gly  
 85 90 95  
 Phe Lys Leu Val Tyr Asp Thr Asn Arg Asn Phe Gln Asn Val Gly Phe  
 100 105 110  
 Arg Ser Gln Ser Met Ile Met Thr Thr Phe Pro Leu Tyr Tyr Arg Gly  
 115 120 125  
 Trp Tyr Asn Pro Glu Thr Asn Thr Tyr Ser Leu Glu Asp Ser Thr Pro  
 130 135 140  
 His Gly Ser Leu Leu Gly Arg Asn Gly Val Thr Leu Asn Ile Arg Gln  
 145 150 155 160  
 Val Phe Trp Trp Asp Asn Phe Asn Trp Ser Ile Gly Phe Tyr Asn Thr  
 165 170 175  
 Phe Gly Asn Ser Asp Ala Phe Leu Gly Ser His Thr Met Pro Arg Gly  
 180 185 190  
 Asn Asn Thr Ser Tyr Ile Gly Ser Glu Ile Ser Ile Thr Thr Arg His  
 195 200 205  
 Ala Gly Met Ile Gly Tyr Asp Phe Trp Asp Asn Thr Ala Tyr Asp Gly  
 210 215 220  
 Leu Ala Asp Ala Ile Thr Asn Ala Asn Thr Phe Thr Phe Tyr Thr Ser  
 225 230 235 240  
 Val Gly Gly Ile His Lys Arg Phe Ala Trp His Val Phe Gly Arg Val  
 245 250 255  
 Ser His Ala Asn Lys Asn Ala Leu Gly Gln Val Gly Arg Ala Asn Glu  
 260 265 270  
 Tyr Ser Leu Gln Phe Asn Ala Ser Tyr Ala Phe Thr Glu Ser Ile Leu  
 275 280 285  
 Leu Asn Phe Arg Ile Thr Tyr Tyr Gly Ala Arg Ile Asn Lys Gly Tyr  
 290 295 300  
 Gln Ala Gly Tyr Phe Gly Ala Pro Lys Phe Asn Asn Pro Asp Gly Asp



gct ttg att ggc gcg att aaa atg gag act aaa agt gct agc gat ttt 651  
Ala Leu Ile Gly Ala Ile Lys Met Glu Thr Lys Ser Ala Ser Asp Phe  
160 165 170  
  
atc cct aaa ggt aaa gac tac gcc ata agt ggg gct gcc act ttt tta 699  
Ile Pro Lys Gly Lys Asp Tyr Ala Ile Ser Gly Ala Ala Thr Phe Leu  
175 180 185  
  
acc aac ttt ggg gat cga gaa acc gtg atg ggc gct tat cgt cat aat 747  
Thr Asn Phe Gly Asp Arg Glu Thr Val Met Gly Ala Tyr Arg His Asn  
190 195 200 205  
  
cat ttt gat gcg ctt ttg tat tac acg cat caa aat att ttt tac tat 795  
His Phe Asp Ala Leu Leu Tyr Tyr Thr His Gln Asn Ile Phe Tyr Tyr  
210 215 220  
  
cgt gat ggg gat aat gct aca aaa gat ctc ttt aga cct aaa gcg gag 843  
Arg Asp Gly Asp Asn Ala Thr Lys Asp Leu Phe Arg Pro Lys Ala Glu  
225 230 235  
  
aat aaa gtt aca gaa gtc cta gcg agc aaa aca atg tgatggctaa 889  
Asn Lys Val Thr Glu Val Leu Ala Ser Lys Thr Met  
240 245  
  
gatcaatggt tatttgagcg aaagggatat tttaacgctc agttataaca tgaccagaga 949  
caacgctaac 959

<210> 20  
<211> 249  
<212> PRT  
<213> Helicobacter pylori

<400> 20  
Met Asn Asp Lys Arg Phe Arg Lys Tyr Cys Ser Phe Ser Ile Phe Leu  
1 5 10 15  
Ser Leu Leu Gly Thr Phe Glu Leu Glu Ala Lys Glu Glu Glu Glu Lys  
20 25 30  
Glu Glu Arg Lys Thr Glu Arg Lys Lys Glu Lys Asn Ala Gln His Thr  
35 40 45  
Leu Gly Lys Val Thr Thr Gln Ala Ala Lys Ile Phe Asn Tyr Asn Asn  
50 55 60  
Gln Thr Thr Ile Ser Ser Lys Glu Leu Glu Arg Arg Gln Ala Asn Gln  
65 70 75 80  
Ile Ser Asp Met Phe Arg Arg Asn Pro Asn Ile Asn Val Gly Gly Gly  
85 90 95  
Ala Val Ile Ala Gln Lys Ile Tyr Val Arg Gly Ile Glu Asp Arg Leu  
100 105 110  
Ala Arg Val Thr Val Asp Gly Ala Ala Gln Met Gly Ala Ser Tyr Gly  
115 120 125  
His Gln Gly Asn Thr Ile Ile Asp Pro Gly Met Leu Lys Ser Val Val  
130 135 140  
Val Thr Lys Gly Ala Ala Gln Ala Ser Ala Gly Pro Met Ala Leu Ile  
145 150 155 160  
Gly Ala Ile Lys Met Glu Thr Lys Ser Ala Ser Asp Phe Ile Pro Lys  
165 170 175  
Gly Lys Asp Tyr Ala Ile Ser Gly Ala Ala Thr Phe Leu Thr Asn Phe  
180 185 190  
Gly Asp Arg Glu Thr Val Met Gly Ala Tyr Arg His Asn His Phe Asp  
195 200 205

Ala Leu Leu Tyr Tyr Thr His Gln Asn Ile Phe Tyr Tyr Arg Asp Gly  
 210 215 220  
 Asp Asn Ala Thr Lys Asp Leu Phe Arg Pro Lys Ala Glu Asn Lys Val  
 225 230 235 240  
 Thr Glu Val Leu Ala Ser Lys Thr Met  
 245

<210> 21  
 <211> 1397  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (138)...(1244)

<400> 21  
 tgaatgcggg cattggggct aggtttgggc ttgattataa agatattaat atcaccggaa 60  
 atattggtat gcgctatgct ttttaatggt atcattaaac ctatttttaa caatcccaat 120  
 tcatagcagg atcacc atg caa ttt caa aaa gcc tta tta cat tca tca 170  
 Met Gln Phe Gln Lys Ala Leu Leu His Ser Ser  
 1 5 10  
 ttc ttt tta cct tta ttt tta tct ttt tgt atc gct gaa gaa aat ggg 218  
 Phe Phe Leu Pro Leu Phe Leu Ser Phe Cys Ile Ala Glu Glu Asn Gly  
 15 20 25  
 gcg tat gcg agc gtg ggt ttt gaa tat tcc att agt cat gcc gtt gaa 266  
 Ala Tyr Ala Ser Val Gly Phe Glu Tyr Ser Ile Ser His Ala Val Glu  
 30 35 40  
 cac aat aac ccc ttt tta aat caa gaa cgc atc caa atc att tct aac 314  
 His Asn Asn Pro Phe Leu Asn Gln Glu Arg Ile Gln Ile Ile Ser Asn  
 45 50 55  
 gct caa aat aaa atc tat aaa ctc cat caa gtt aaa aat gaa atc aca 362  
 Ala Gln Asn Lys Ile Tyr Lys Leu His Gln Val Lys Asn Glu Ile Thr  
 60 65 70 75  
 agc atg cct aaa acc ttt gca tat atc aac aac gct tta aaa aac aac 410  
 Ser Met Pro Lys Thr Phe Ala Tyr Ile Asn Asn Ala Leu Lys Asn Asn  
 80 85 90  
 tcc aaa tta acc ccc act gaa atg caa gcc gaa caa tac tac ctc caa 458  
 Ser Lys Leu Thr Pro Thr Glu Met Gln Ala Glu Gln Tyr Tyr Leu Gln  
 95 100 105  
 tcc acc ttt caa aac att gaa aaa ata gta atg ctt agc ggt ggc gtt 506  
 Ser Thr Phe Gln Asn Ile Glu Lys Ile Val Met Leu Ser Gly Gly Val  
 110 115 120  
 tca tct aac cca caa tta gtc caa gcg ttg gaa aaa atg caa gaa ccc 554  
 Ser Ser Asn Pro Gln Leu Val Gln Ala Leu Glu Lys Met Gln Glu Pro  
 125 130 135  
 att act aac cct tta gaa ttt gaa gaa aac tta aga aat tta gaa gtg 602  
 Ile Thr Asn Pro Leu Glu Phe Glu Glu Asn Leu Arg Asn Leu Glu Val  
 140 145 150 155

caa ttt gct caa tct caa aac cgc atg ctt tct tct tta tct tct caa	650
Gln Phe Ala Gln Ser Gln Asn Arg Met Leu Ser Ser Leu Ser Ser Gln	
160 165 170	
atc gct gcc att tca aat tcc tta aac gcg ctt gat cct aac tct tat	698
Ile Ala Ala Ile Ser Asn Ser Leu Asn Ala Leu Asp Pro Asn Ser Tyr	
175 180 185	
tct aaa aac att tca agc atg tat ggg gtg agt ttg agc gta ggt tat	746
Ser Lys Asn Ile Ser Ser Met Tyr Gly Val Ser Leu Ser Val Gly Tyr	
190 195 200	
aag cat ttc ttt acc aag aaa aaa aat caa ggg ttg cgc tat tac ttg	794
Lys His Phe Phe Thr Lys Lys Lys Asn Gln Gly Leu Arg Tyr Tyr Leu	
205 210 215	
ttt tat gac tat ggt tac act aat ttt ggt ttt gtg ggc aat ggc ttt	842
Phe Tyr Asp Tyr Gly Tyr Thr Asn Phe Gly Phe Val Gly Asn Gly Phe	
220 225 230 235	
gat ggt tta ggc aaa atg aat aac cat ctc tat ggg ctt ggg ata gac	890
Asp Gly Leu Gly Lys Met Asn Asn His Leu Tyr Gly Leu Gly Ile Asp	
240 245 250	
tat ctt tat aat ttc att gat aat gca aaa aaa cac tct agc gta ggt	938
Tyr Leu Tyr Asn Phe Ile Asp Asn Ala Lys Lys His Ser Ser Val Gly	
255 260 265	
ttt tat ctg ggt ttt gct tta gcg ggg agt tcg tgg gta ggg agt ggt	986
Phe Tyr Leu Gly Phe Ala Leu Ala Gly Ser Ser Trp Val Gly Ser Gly	
270 275 280	
ttg agc atg tgg gtg agc caa acg gat ttt atc aac aat tac ttg acg	1034
Leu Ser Met Trp Val Ser Gln Thr Asp Phe Ile Asn Asn Tyr Leu Thr	
285 290 295	
ggc tat caa gct aaa atg cac acg agt ttt ttc cag atc cct ttg aat	1082
Gly Tyr Gln Ala Lys Met His Thr Ser Phe Phe Gln Ile Pro Leu Asn	
300 305 310 315	
ttt ggg gtt cgt gtg aat gtc aat agg cat aat ggc ttt gaa atg ggc	1130
Phe Gly Val Arg Val Asn Val Asn Arg His Asn Gly Phe Glu Met Gly	
320 325 330	
ttg aaa atc cct tta gcg atg aat tcc ttt tat gaa acg cat ggc aaa	1178
Leu Lys Ile Pro Leu Ala Met Asn Ser Phe Tyr Glu Thr His Gly Lys	
335 340 345	
ggg cta aac act tcc ctc ttt ttc aaa cgc ctt gtc atg ttt aac gtg	1226
Gly Leu Asn Thr Ser Leu Phe Phe Lys Arg Leu Val Met Phe Asn Val	
350 355 360	
agt tac gtt tat agt ttt taggggggta gaaataagca ccccttaaa	1274
Ser Tyr Val Tyr Ser Phe	
365	
tgttatcgca acctttgaat tttaaaaact ctttagtttt tttgcctcaa atgatggacg	1334
ctctcgcccc caagaccata attattagaa tcgacctcat ctataatgac cacaatagaa	1394

gcc

1397

<210> 22  
 <211> 369  
 <212> PRT  
 <213> Helicobacter pylori

<400> 22  
 Met Gln Phe Gln Lys Ala Leu Leu His Ser Ser Phe Phe Leu Pro Leu  
 1 5 10 15  
 Phe Leu Ser Phe Cys Ile Ala Glu Glu Asn Gly Ala Tyr Ala Ser Val  
 20 25 30  
 Gly Phe Glu Tyr Ser Ile Ser His Ala Val Glu His Asn Asn Pro Phe  
 35 40 45  
 Leu Asn Gln Glu Arg Ile Gln Ile Ile Ser Asn Ala Gln Asn Lys Ile  
 50 55 60  
 Tyr Lys Leu His Gln Val Lys Asn Glu Ile Thr Ser Met Pro Lys Thr  
 65 70 75 80  
 Phe Ala Tyr Ile Asn Asn Ala Leu Lys Asn Asn Ser Lys Leu Thr Pro  
 85 90 95  
 Thr Glu Met Gln Ala Glu Gln Tyr Tyr Leu Gln Ser Thr Phe Gln Asn  
 100 105 110  
 Ile Glu Lys Ile Val Met Leu Ser Gly Gly Val Ser Ser Asn Pro Gln  
 115 120 125  
 Leu Val Gln Ala Leu Glu Lys Met Gln Glu Pro Ile Thr Asn Pro Leu  
 130 135 140  
 Glu Phe Glu Glu Asn Leu Arg Asn Leu Glu Val Gln Phe Ala Gln Ser  
 145 150 155 160  
 Gln Asn Arg Met Leu Ser Ser Leu Ser Ser Gln Ile Ala Ala Ile Ser  
 165 170 175  
 Asn Ser Leu Asn Ala Leu Asp Pro Asn Ser Tyr Ser Lys Asn Ile Ser  
 180 185 190  
 Ser Met Tyr Gly Val Ser Leu Ser Val Gly Tyr Lys His Phe Phe Thr  
 195 200 205  
 Lys Lys Lys Asn Gln Gly Leu Arg Tyr Tyr Leu Phe Tyr Asp Tyr Gly  
 210 215 220  
 Tyr Thr Asn Phe Gly Phe Val Gly Asn Gly Phe Asp Gly Leu Gly Lys  
 225 230 235 240  
 Met Asn Asn His Leu Tyr Gly Leu Gly Ile Asp Tyr Leu Tyr Asn Phe  
 245 250 255  
 Ile Asp Asn Ala Lys Lys His Ser Ser Val Gly Phe Tyr Leu Gly Phe  
 260 265 270  
 Ala Leu Ala Gly Ser Ser Trp Val Gly Ser Gly Leu Ser Met Trp Val  
 275 280 285  
 Ser Gln Thr Asp Phe Ile Asn Asn Tyr Leu Thr Gly Tyr Gln Ala Lys  
 290 295 300  
 Met His Thr Ser Phe Phe Gln Ile Pro Leu Asn Phe Gly Val Arg Val  
 305 310 315 320  
 Asn Val Asn Arg His Asn Gly Phe Glu Met Gly Leu Lys Ile Pro Leu  
 325 330 335  
 Ala Met Asn Ser Phe Tyr Glu Thr His Gly Lys Gly Leu Asn Thr Ser  
 340 345 350  
 Leu Phe Phe Lys Arg Leu Val Met Phe Asn Val Ser Tyr Val Tyr Ser  
 355 360 365  
 Phe

<210> 23



<211> 1030  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (342)...(824)

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agccttacaa aatatcttaa ataacgctaa aagcgcgcat tttaaatttg ttttagagag 120
ccaaaacgcc gctcaatcta ttatagaaat tcaaagcctc ttgaaacaac tctccttaaa 180
aaataatgaa atcttttttaa tgccttttagg cacaaataac aacgagctag acaaaaaatct 240
aaaaacccta gcccccttag ccataaagca tggtttcagg ctaagcgata ggcttcatat 300
ccgcttggtg gataatcaaa aagggtttta aaaagttaat c atg acc atc aaa gtt 356
                                         Met Thr Ile Lys Val
                                         1           5

ttt tcg ccc aaa tac ccc act gaa tta gaa gaa ttt tat gct gag cgt 404
Phe Ser Pro Lys Tyr Pro Thr Glu Leu Glu Glu Phe Tyr Ala Glu Arg
                        10                        15                        20

atc gct gac aac cct tta ggg ttt atc caa cgc ttg gat ctt ttg cct 452
Ile Ala Asp Asn Pro Leu Gly Phe Ile Gln Arg Leu Asp Leu Leu Pro
                        25                        30                        35

agt att agc ggg ttc gtt caa aaa ttg cgc gag cat ggc ggg gaa ttt 500
Ser Ile Ser Gly Phe Val Gln Lys Leu Arg Glu His Gly Gly Glu Phe
                        40                        45                        50

ttt gaa atg aga gag ggt aac aag ctc att ggg att tgt ggg ctt aat 548
Phe Glu Met Arg Glu Gly Asn Lys Leu Ile Gly Ile Cys Gly Leu Asn
                        55                        60                        65

cct atc aat caa aca gaa gcc gag ctg tgc aaa ttc cac ata aat agt 596
Pro Ile Asn Gln Thr Glu Ala Glu Leu Cys Lys Phe His Ile Asn Ser
                        70                        75                        80                        85

gct tat caa tcc caa ggg cta ggt caa aaa ctc tat gag agc gtg gag 644
Ala Tyr Gln Ser Gln Gly Leu Gly Gln Lys Leu Tyr Glu Ser Val Glu
                        90                        95                        100

aaa tac gct ttc att aaa ggc tat act aaa atc tct ctg cat gtg agc 692
Lys Tyr Ala Phe Ile Lys Gly Tyr Thr Lys Ile Ser Leu His Val Ser
                        105                        110                        115

aaa agc caa atc aag gca tgc aac ctc tat caa aag ctg ggt ttt gtg 740
Lys Ser Gln Ile Lys Ala Cys Asn Leu Tyr Gln Lys Leu Gly Phe Val
                        120                        125                        130

cac atc aaa gaa gag gat tgc gtg gtg gag ttg ggc gaa gag act ttg 788
His Ile Lys Glu Glu Asp Cys Val Val Glu Leu Gly Glu Glu Thr Leu
                        135                        140                        145

att ttc ccc act ctt ttt atg gaa aag att ttg tct tgattggtgc 834
Ile Phe Pro Thr Leu Phe Met Glu Lys Ile Leu Ser
150                        155                        160

atccatttga cacacgccca agcgacattc aaactatcaa actttcatta acacaaccca 894

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attaacgcta aataaacctt aaaacaaaca ctcggttgta aaattttgtt tttcaagcgc 954  
 ttcgcaaagt tttagaagcc ctatttaggg gttacgcta aaataggcta tcaaaactac 1014  
 tttaatgatt ttatag 1030

<210> 24  
 <211> 161  
 <212> PRT  
 <213> Helicobacter pylori

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 Phe Tyr Ala Glu Arg Ile Ala Asp Asn Pro Leu Gly Phe Ile Gln Arg  
 20 25 30  
 Leu Asp Leu Leu Pro Ser Ile Ser Gly Phe Val Gln Lys Leu Arg Glu  
 35 40 45  
 His Gly Gly Glu Phe Phe Glu Met Arg Glu Gly Asn Lys Leu Ile Gly  
 50 55 60  
 Ile Cys Gly Leu Asn Pro Ile Asn Gln Thr Glu Ala Glu Leu Cys Lys  
 65 70 75 80  
 Phe His Ile Asn Ser Ala Tyr Gln Ser Gln Gly Leu Gly Gln Lys Leu  
 85 90 95  
 Tyr Glu Ser Val Glu Lys Tyr Ala Phe Ile Lys Gly Tyr Thr Lys Ile  
 100 105 110  
 Ser Leu His Val Ser Lys Ser Gln Ile Lys Ala Cys Asn Leu Tyr Gln  
 115 120 125  
 Lys Leu Gly Phe Val His Ile Lys Glu Glu Asp Cys Val Val Glu Leu  
 130 135 140  
 Gly Glu Glu Thr Leu Ile Phe Pro Thr Leu Phe Met Glu Lys Ile Leu  
 145 150 155 160  
 Ser

<210> 25  
 <211> 1477  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (374)...(1267)

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 caactaaaat ctctactaac aattcatctg aatgcaaaat ctcaattctc cctaaaaaac 120  
 aaaatcactt ttaagactaa atcatgttag aattatactt gaattttacac tcagtttagt 180  
 ttattttctta atacaaaagg taggcgtttt gaaacattta accccactca ctacacccat 240  
 ctttaaagcc ttatggctag gcacagcctt aagtgcattt ttaagttagt ccgcaacaga 300  
 aagccccact aaaacagagc ctaagccgcg taaaggggtt aaaaacaagc ccaaactcgc 360  
 cgttactaaa gtc atg acc aat tgc gac aat att aaa gat ttt aac 409  
 Met Met Thr Asn Cys Asp Asn Ile Lys Asp Phe Asn  
 1 5 10  
 gct aag caa aaa gaa gtc tta aaa gcc gct tat caa ttc ggc tct aaa 457  
 Ala Lys Gln Lys Glu Val Leu Lys Ala Ala Tyr Gln Phe Gly Ser Lys  
 15 20 25  
 gaa aat tta ggc tat gaa atg gca ggc att gca tgg aaa gag tca tgc 505

Glu	Asn	Leu	Gly	Tyr	Glu	Met	Ala	Gly	Ile	Ala	Trp	Lys	Glu	Ser	Cys	
30						35					40					
gca	ggg	gtt	tat	aaa	atc	aat	ttt	tcg	gat	ccg	agc	gcg	ggc	gtg	tat	553
Ala	Gly	Val	Tyr	Lys	Ile	Asn	Phe	Ser	Asp	Pro	Ser	Ala	Gly	Val	Tyr	
45					50				55						60	
cat	tct	tat	atc	cca	agc	gtt	cta	aaa	agc	tat	ggg	cat	aat	gat	agc	601
His	Ser	Tyr	Ile	Pro	Ser	Val	Leu	Lys	Ser	Tyr	Gly	His	Asn	Asp	Ser	
				65					70					75		
ccc	ttt	ttg	cgt	aat	gtg	atg	ggg	gaa	ttg	ctc	att	aaa	gac	gat	gcg	649
Pro	Phe	Leu	Arg	Asn	Val	Met	Gly	Glu	Leu	Leu	Ile	Lys	Asp	Asp	Ala	
			80					85					90			
ttt	gct	tct	gaa	gtg	gct	tta	aaa	gag	ttg	ctc	tat	tgg	aaa	aca	cgc	697
Phe	Ala	Ser	Glu	Val	Ala	Leu	Lys	Glu	Leu	Leu	Tyr	Trp	Lys	Thr	Arg	
		95					100					105				
tac	cat	gac	aat	tta	aaa	gac	atg	att	aaa	tct	tac	aac	aag	ggc	agt	745
Tyr	His	Asp	Asn	Leu	Lys	Asp	Met	Ile	Lys	Ser	Tyr	Asn	Lys	Gly	Ser	
	110					115					120					
cgt	tgg	gaa	agg	agc	gaa	aaa	tct	aac	gct	gat	gct	gaa	aaa	tat	tac	793
Arg	Trp	Glu	Arg	Ser	Glu	Lys	Ser	Asn	Ala	Asp	Ala	Glu	Lys	Tyr	Tyr	
125					130					135					140	
gaa	gag	ata	caa	gac	aga	atc	agg	cgt	ttg	aaa	gaa	tct	aaa	atc	ttt	841
Glu	Glu	Ile	Gln	Asp	Arg	Ile	Arg	Arg	Leu	Lys	Glu	Ser	Lys	Ile	Phe	
				145					150					155		
gat	tcg	cag	tct	agt	aat	gac	caa	gaa	ttg	caa	aaa	agc	gct	aat	agc	889
Asp	Ser	Gln	Ser	Ser	Asn	Asp	Gln	Glu	Leu	Gln	Lys	Ser	Ala	Asn	Ser	
			160					165					170			
aac	ctg	gat	tta	gac	cct	atc	ggc	aac	gcc	atg	ccc	caa	gcc	tta	att	937
Asn	Leu	Asp	Leu	Asp	Pro	Ile	Gly	Asn	Ala	Met	Pro	Gln	Ala	Leu	Ile	
		175					180					185				
gcc	aaa	gaa	act	aaa	ata	gaa	gaa	acc	caa	gca	gaa	aaa	tcc	caa	gaa	985
Ala	Lys	Glu	Thr	Lys	Ile	Glu	Glu	Thr	Gln	Ala	Glu	Lys	Ser	Gln	Glu	
	190					195					200					
atg	aaa	gag	aca	act	agc	gag	caa	aca	aaa	agt	aag	cca	gaa	aaa	gca	1033
Met	Lys	Glu	Thr	Thr	Ser	Glu	Gln	Thr	Lys	Ser	Lys	Pro	Glu	Lys	Ala	
205					210					215					220	
aaa	gat	aaa	ccc	atg	tat	ttg	gcg	caa	atc	aac	agc	act	gat	ttc	aca	1081
Lys	Asp	Lys	Pro	Met	Tyr	Leu	Ala	Gln	Ile	Asn	Ser	Thr	Asp	Phe	Thr	
				225					230					235		
ccc	gtt	aaa	aaa	agc	ccc	aaa	aaa	ccg	gct	aaa	gtg	agc	caa	aaa	cac	1129
Pro	Val	Lys	Lys	Ser	Pro	Lys	Lys	Pro	Ala	Lys	Val	Ser	Gln	Lys	His	
			240					245					250			
tcc	ttt	aag	aat	aac	att	aaa	aat	aat	gta	aaa	aac	aac	gcc	aaa	acc	1177
Ser	Phe	Lys	Asn	Asn	Ile	Lys	Asn	Asn	Val	Lys	Asn	Asn	Ala	Lys	Thr	
		255					260					265				

gct tcc aaa aaa caa gaa atg tgc aaa aat tgc tct cca ggg caa agg 1225  
 Ala Ser Lys Lys Gln Glu Met Cys Lys Asn Cys Ser Pro Gly Gln Arg  
 270 275 280

aat gcg att tta gct aac cac atc act ctc atg caa gag ctt 1267  
 Asn Ala Ile Leu Ala Asn His Ile Thr Leu Met Gln Glu Leu  
 285 290 295

taaaaagtcc taaaaatggc gcaaaaaaact cttttgatta tcactgatgg cattgggtat 1327  
 cgtaaagata gcgatcataa cgctttcttc catgccaaaa aaccactta tgatttgatg 1387  
 tttaaaacct tgccttatag cctgattgat acgcatggct tgagcgtggg cttacctaag 1447  
 gggcaaatgg gaaattctga agtggggcat 1477

<210> 26  
 <211> 298  
 <212> PRT  
 <213> Helicobacter pylori

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 Met Met Thr Asn Cys Asp Asn Ile Lys Asp Phe Asn Ala Lys Gln Lys  
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 Tyr Glu Met Ala Gly Ile Ala Trp Lys Glu Ser Cys Ala Gly Val Tyr  
 35 40 45  
 Lys Ile Asn Phe Ser Asp Pro Ser Ala Gly Val Tyr His Ser Tyr Ile  
 50 55 60  
 Pro Ser Val Leu Lys Ser Tyr Gly His Asn Asp Ser Pro Phe Leu Arg  
 65 70 75 80  
 Asn Val Met Gly Glu Leu Leu Ile Lys Asp Asp Ala Phe Ala Ser Glu  
 85 90 95  
 Val Ala Leu Lys Glu Leu Leu Tyr Trp Lys Thr Arg Tyr His Asp Asn  
 100 105 110  
 Leu Lys Asp Met Ile Lys Ser Tyr Asn Lys Gly Ser Arg Trp Glu Arg  
 115 120 125  
 Ser Glu Lys Ser Asn Ala Asp Ala Glu Lys Tyr Tyr Glu Glu Ile Gln  
 130 135 140  
 Asp Arg Ile Arg Arg Leu Lys Glu Ser Lys Ile Phe Asp Ser Gln Ser  
 145 150 155 160  
 Ser Asn Asp Gln Glu Leu Gln Lys Ser Ala Asn Ser Asn Leu Asp Leu  
 165 170 175  
 Asp Pro Ile Gly Asn Ala Met Pro Gln Ala Leu Ile Ala Lys Glu Thr  
 180 185 190  
 Lys Ile Glu Glu Thr Gln Ala Glu Lys Ser Gln Glu Met Lys Glu Thr  
 195 200 205  
 Thr Ser Glu Gln Thr Lys Ser Lys Pro Glu Lys Ala Lys Asp Lys Pro  
 210 215 220  
 Met Tyr Leu Ala Gln Ile Asn Ser Thr Asp Phe Thr Pro Val Lys Lys  
 225 230 235 240  
 Ser Pro Lys Lys Pro Ala Lys Val Ser Gln Lys His Ser Phe Lys Asn  
 245 250 255  
 Asn Ile Lys Asn Asn Val Lys Asn Asn Ala Lys Thr Ala Ser Lys Lys  
 260 265 270  
 Gln Glu Met Cys Lys Asn Cys Ser Pro Gly Gln Arg Asn Ala Ile Leu  
 275 280 285  
 Ala Asn His Ile Thr Leu Met Gln Glu Leu  
 290 295

<210> 27  
 <211> 1515  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (141)...(1340)

<400> 27  
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 atgggggtgt atttgattta tggcatcatt cggtagctct ttttaatggt aaaaattatt 120  
 ttttaataaaa ataaaagcgc atg aaa gaa tct ttt tac ata gag gga atg act 173  
 Met Lys Glu Ser Phe Tyr Ile Glu Gly Met Thr  
 1 5 10

tgc acg gcg tgt tct agc ggg att gaa cgc tct ttg ggg cgt aag agt 221  
 Cys Thr Ala Cys Ser Ser Gly Ile Glu Arg Ser Leu Gly Arg Lys Ser  
 15 20 25

ttt gtg aaa aaa ata gaa gtg agc ctt tta aat aag agc gct aac att 269  
 Phe Val Lys Lys Ile Glu Val Ser Leu Leu Asn Lys Ser Ala Asn Ile  
 30 35 40

gaa ttt gac gaa aac caa acc aat tta gac gaa att ttt aaa ctc att 317  
 Glu Phe Asp Glu Asn Gln Thr Asn Leu Asp Glu Ile Phe Lys Leu Ile  
 45 50 55

gaa aag cta ggc tat agc cct aaa aaa gct ctg aca aaa gaa aaa aaa 365  
 Glu Lys Leu Gly Tyr Ser Pro Lys Lys Ala Leu Thr Lys Glu Lys Lys  
 60 65 70 75

gaa ttt ttt agc cct aat gtt aaa tta gcg tta gcg gtt att ttc acg 413  
 Glu Phe Phe Ser Pro Asn Val Lys Leu Ala Leu Ala Val Ile Phe Thr  
 80 85 90

ctt ttt gtg gtg tat ctt tct atg ggg gcg atg ctt agc cct agc ctt 461  
 Leu Phe Val Val Tyr Leu Ser Met Gly Ala Met Leu Ser Pro Ser Leu  
 95 100 105

tta cct gaa agc ttg ctt gca att gat aat cat agt aat ttt tta aac 509  
 Leu Pro Glu Ser Leu Leu Ala Ile Asp Asn His Ser Asn Phe Leu Asn  
 110 115 120

gct tgc tta cag ctt ata ggc gca ctc att gtc atg cat ttg ggg agg 557  
 Ala Cys Leu Gln Leu Ile Gly Ala Leu Ile Val Met His Leu Gly Arg  
 125 130 135

gat ttt tac att caa ggg ttt aaa gcc tta tgg cac aga caa ccc aac 605  
 Asp Phe Tyr Ile Gln Gly Phe Lys Ala Leu Trp His Arg Gln Pro Asn  
 140 145 150 155

atg agc agc ctt atc gcc ata ggc aca agc gct gcc tta att tca agc 653  
 Met Ser Ser Leu Ile Ala Ile Gly Thr Ser Ala Ala Leu Ile Ser Ser  
 160 165 170

ctg tgg caa ttg tat ttg gtc tat acc aat cat tat acc gat cag tgg 701  
 Leu Trp Gln Leu Tyr Leu Val Tyr Thr Asn His Tyr Thr Asp Gln Trp  
 175 180 185

tct tat ggg cat tat tat ttt gaa agc gtg tgc gtg att tta atg ttt	749
Ser Tyr Gly His Tyr Tyr Phe Glu Ser Val Cys Val Ile Leu Met Phe	
190 195 200	
gtg atg gtg ggc aaa cgc att gaa aat gtt tct aaa gac aaa gct tta	797
Val Met Val Gly Lys Arg Ile Glu Asn Val Ser Lys Asp Lys Ala Leu	
205 210 215	
gac gct atg caa gcc ttg atg aaa aac gcc cca aaa acc gcc ctt aaa	845
Asp Ala Met Gln Ala Leu Met Lys Asn Ala Pro Lys Thr Ala Leu Lys	
220 225 230 235	
atg caa aat aac caa cag att gaa gtt tta gtg gat agc att gtg gtg	893
Met Gln Asn Asn Gln Gln Ile Glu Val Leu Val Asp Ser Ile Val Val	
240 245 250	
ggg gat att cta aaa gtc ctc cct gga agc gcg att gcg gtg gat ggt	941
Gly Asp Ile Leu Lys Val Leu Pro Gly Ser Ala Ile Ala Val Asp Gly	
255 260 265	
gaa atc ata gag ggc gaa ggg gaa tta gat gag agc atg ttg agc ggc	989
Glu Ile Ile Glu Gly Glu Gly Glu Leu Asp Glu Ser Met Leu Ser Gly	
270 275 280	
gaa gcg ttg ccg gtt tat aaa aaa gtc ggc gat aaa gtc ttt tca ggg	1037
Glu Ala Leu Pro Val Tyr Lys Lys Val Gly Asp Lys Val Phe Ser Gly	
285 290 295	
aca ttc aat agc cac acg agt ttt tta atg aaa gcc acg caa aac aac	1085
Thr Phe Asn Ser His Thr Ser Phe Leu Met Lys Ala Thr Gln Asn Asn	
300 305 310 315	
aaa aac agc acc ttg tct caa att ata gaa atg att tat aac gct caa	1133
Lys Asn Ser Thr Leu Ser Gln Ile Ile Glu Met Ile Tyr Asn Ala Gln	
320 325 330	
agt tca aag gca gag att tct cgc tta gcg gat aag gtt tca agc gtg	1181
Ser Ser Lys Ala Glu Ile Ser Arg Leu Ala Asp Lys Val Ser Ser Val	
335 340 345	
ttt gtg cca agc gtg atc gct att tct att tta gcg ttt gtg gtg tgg	1229
Phe Val Pro Ser Val Ile Ala Ile Ser Ile Leu Ala Phe Val Val Trp	
350 355 360	
ctc atc att gca cct aag ccc gat ttt tgg tgg aat ttt gga atc gct	1277
Leu Ile Ile Ala Pro Lys Pro Asp Phe Trp Trp Asn Phe Gly Ile Ala	
365 370 375	
tta gaa gtg ttt gta tgc gtt tta gtg att tct tgc cct tgc gct tta	1325
Leu Glu Val Phe Val Ser Val Leu Val Ile Ser Cys Pro Cys Ala Leu	
380 385 390 395	
gga ttg cta cgc cta tgagcatttt agtagcgaac cagaaagcga gttcttttagg	1380
Gly Leu Leu Arg Leu	
400	
ggtatttttt aaagacgcta aaagttaga aaaagcaagg ctagtcaata cgatcgTTTT	1440
tgataaaacc ggcacgctca ctaacggcaa gcctgtcgTTT aaaagcgTTC attctaagat	1500

agaattatta gagtt

1515

<210> 28  
<211> 400  
<212> PRT  
<213> Helicobacter pylori

<400> 28  
Met Lys Glu Ser Phe Tyr Ile Glu Gly Met Thr Cys Thr Ala Cys Ser  
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Ser Gly Ile Glu Arg Ser Leu Gly Arg Lys Ser Phe Val Lys Lys Ile  
20 25 30  
Glu Val Ser Leu Leu Asn Lys Ser Ala Asn Ile Glu Phe Asp Glu Asn  
35 40 45  
Gln Thr Asn Leu Asp Glu Ile Phe Lys Leu Ile Glu Lys Leu Gly Tyr  
50 55 60  
Ser Pro Lys Lys Ala Leu Thr Lys Glu Lys Lys Glu Phe Phe Ser Pro  
65 70 75 80  
Asn Val Lys Leu Ala Leu Ala Val Ile Phe Thr Leu Phe Val Val Tyr  
85 90 95  
Leu Ser Met Gly Ala Met Leu Ser Pro Ser Leu Leu Pro Glu Ser Leu  
100 105 110  
Leu Ala Ile Asp Asn His Ser Asn Phe Leu Asn Ala Cys Leu Gln Leu  
115 120 125  
Ile Gly Ala Leu Ile Val Met His Leu Gly Arg Asp Phe Tyr Ile Gln  
130 135 140  
Gly Phe Lys Ala Leu Trp His Arg Gln Pro Asn Met Ser Ser Leu Ile  
145 150 155 160  
Ala Ile Gly Thr Ser Ala Ala Leu Ile Ser Ser Leu Trp Gln Leu Tyr  
165 170 175  
Leu Val Tyr Thr Asn His Tyr Thr Asp Gln Trp Ser Tyr Gly His Tyr  
180 185 190  
Tyr Phe Glu Ser Val Cys Val Ile Leu Met Phe Val Met Val Gly Lys  
195 200 205  
Arg Ile Glu Asn Val Ser Lys Asp Lys Ala Leu Asp Ala Met Gln Ala  
210 215 220  
Leu Met Lys Asn Ala Pro Lys Thr Ala Leu Lys Met Gln Asn Asn Gln  
225 230 235 240  
Gln Ile Glu Val Leu Val Asp Ser Ile Val Val Gly Asp Ile Leu Lys  
245 250 255  
Val Leu Pro Gly Ser Ala Ile Ala Val Asp Gly Glu Ile Ile Glu Gly  
260 265 270  
Glu Gly Glu Leu Asp Glu Ser Met Leu Ser Gly Glu Ala Leu Pro Val  
275 280 285  
Tyr Lys Lys Val Gly Asp Lys Val Phe Ser Gly Thr Phe Asn Ser His  
290 295 300  
Thr Ser Phe Leu Met Lys Ala Thr Gln Asn Asn Lys Asn Ser Thr Leu  
305 310 315 320  
Ser Gln Ile Ile Glu Met Ile Tyr Asn Ala Gln Ser Ser Lys Ala Glu  
325 330 335  
Ile Ser Arg Leu Ala Asp Lys Val Ser Ser Val Phe Val Pro Ser Val  
340 345 350  
Ile Ala Ile Ser Ile Leu Ala Phe Val Val Trp Leu Ile Ile Ala Pro  
355 360 365  
Lys Pro Asp Phe Trp Trp Asn Phe Gly Ile Ala Leu Glu Val Phe Val  
370 375 380  
Ser Val Leu Val Ile Ser Cys Pro Cys Ala Leu Gly Leu Leu Arg Leu  
385 390 395 400

<210> 29  
 <211> 1443  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (76)...(1389)

<400> 29  
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 tagtagagag atggg atg aaa aaa ata tgg ctt tta gtg tgg ggc ttg tgt 111  
 Met Lys Lys Ile Trp Leu Leu Val Trp Gly Leu Cys  
 1 5 10

tct tgg gtg ttt ttg cat gcg ata gag atg ata gaa aaa gcc cct aca 159  
 Ser Trp Val Phe Leu His Ala Ile Glu Met Ile Glu Lys Ala Pro Thr  
 15 20 25

aat gta gag gat aga gac aaa gcc ccc cat ttg ttg ctt tta gca ggg 207  
 Asn Val Glu Asp Arg Asp Lys Ala Pro His Leu Leu Leu Leu Ala Gly  
 30 35 40

att caa ggc gat gag cct ggt ggg ttt aat gca act aat ttg ttt tta 255  
 Ile Gln Gly Asp Glu Pro Gly Gly Phe Asn Ala Thr Asn Leu Phe Leu  
 45 50 55 60

atg cat tat agc gtt tta aaa ggt ttg gtt gaa gtg gtt cct gta ttg 303  
 Met His Tyr Ser Val Leu Lys Gly Leu Val Glu Val Val Pro Val Leu  
 65 70 75

aat aag cct tcc atg tta aga aat cat agg ggc ttg tat ggg gat atg 351  
 Asn Lys Pro Ser Met Leu Arg Asn His Arg Gly Leu Tyr Gly Asp Met  
 80 85 90

aac cgc aaa ttt gcc gct tta gac aag aat gac cct gaa tac ccc act 399  
 Asn Arg Lys Phe Ala Ala Leu Asp Lys Asn Asp Pro Glu Tyr Pro Thr  
 95 100 105

atc cag gaa atc aaa tcc ttg att gca aaa ccc agt ata gac gct gtc 447  
 Ile Gln Glu Ile Lys Ser Leu Ile Ala Lys Pro Ser Ile Asp Ala Val  
 110 115 120

ttg cat ttg cat gat ggc ggt ggg tat tac cgc cct gtt tat gtt gat 495  
 Leu His Leu His Asp Gly Gly Gly Tyr Tyr Arg Pro Val Tyr Val Asp  
 125 130 135 140

gcg atg ctc aat cct aag cgc tgg ggg aat tgc ttt att att gat caa 543  
 Ala Met Leu Asn Pro Lys Arg Trp Gly Asn Cys Phe Ile Ile Asp Gln  
 145 150 155

gat gag gtt aaa ggg gcg aaa ttc cct aat ttg ctt gct ttt gca aac 591  
 Asp Glu Val Lys Gly Ala Lys Phe Pro Asn Leu Leu Ala Phe Ala Asn  
 160 165 170

aat acg att gag agt atc aac gcc cat tta ttg cac ccc att gaa gag 639  
 Asn Thr Ile Glu Ser Ile Asn Ala His Leu Leu His Pro Ile Glu Glu  
 175 180 185



tat cat tta aaa aac acg cgc acc gcg caa ggc gat aca gaa atg caa Tyr His Leu Lys Asn Thr Arg Thr Ala Gln Gly Asp Thr Glu Met Gln 190 195 200	687
aaa gcc cta act ttt tat gcg atc aac caa aaa aag agc gct ttt gcc Lys Ala Leu Thr Phe Tyr Ala Ile Asn Gln Lys Lys Ser Ala Phe Ala 205 210 215 220	735
aat gaa gct agc aaa gaa ctc cct tta gca tca agg gtg ttt tac cac Asn Glu Ala Ser Lys Glu Leu Pro Leu Ala Ser Arg Val Phe Tyr His 225 230 235	783
ctg caa gcc att gag ggc tta ctc aat cag ctc aat atc cct ttt aag Leu Gln Ala Ile Glu Gly Leu Leu Asn Gln Leu Asn Ile Pro Phe Lys 240 245 250	831
cgc gat ttt gat ctt aac cct aac agc gtg cat gcc cta atc aat gat Arg Asp Phe Asp Leu Asn Pro Asn Ser Val His Ala Leu Ile Asn Asp 255 260 265	879
aaa aac ttg tgg gca aaa atc agc tct ttg cct aaa atg ccc ctt ttt Lys Asn Leu Trp Ala Lys Ile Ser Ser Leu Pro Lys Met Pro Leu Phe 270 275 280	927
aac ttg cgc cct aaa ctc aat cat ttc ccc tta ccc cac aac act aaa Asn Leu Arg Pro Lys Leu Asn His Phe Pro Leu Pro His Asn Thr Lys 285 290 295 300	975
atc cca caa atc ccc ata gag agc aac gct tac att gta ggg cta gtc Ile Pro Gln Ile Pro Ile Glu Ser Asn Ala Tyr Ile Val Gly Leu Val 305 310 315	1023
aaa aat aaa caa gaa gtg ttt tta aaa tac ggc aac aag ctc atg aca Lys Asn Lys Gln Glu Val Phe Leu Lys Tyr Gly Asn Lys Leu Met Thr 320 325 330	1071
cga tta tcg cct ttt tac ata gag ttt gat cct tct tta gaa gaa gtg Arg Leu Ser Pro Phe Tyr Ile Glu Phe Asp Pro Ser Leu Glu Glu Val 335 340 345	1119
aaa atg caa att gac aat aag gat caa atg gtt aaa ata ggg agc gtg Lys Met Gln Ile Asp Asn Lys Asp Gln Met Val Lys Ile Gly Ser Val 350 355 360	1167
gtt gaa gtg aaa gag agt ttt tat atc cat gct atg gac aat atc cgt Val Glu Val Lys Glu Ser Phe Tyr Ile His Ala Met Asp Asn Ile Arg 365 370 375 380	1215
gcg aat gtg att ggc ttt agc gtt tct aat gaa aat aag cct aat gaa Ala Asn Val Ile Gly Phe Ser Val Ser Asn Glu Asn Lys Pro Asn Glu 385 390 395	1263
gcg ggt tat acg att aaa ttt aaa gat ttt caa aaa cgc ttt tca ttg Ala Gly Tyr Thr Ile Lys Phe Lys Asp Phe Gln Lys Arg Phe Ser Leu 400 405 410	1311
gac aag caa gaa agg atc tat cgc ata gaa ttt tat aaa aac aac gcg Asp Lys Gln Glu Arg Ile Tyr Arg Ile Glu Phe Tyr Lys Asn Asn Ala 415 420 425	1359

ttt agc ggg atg atc tta gtg aaa ttt gtg taggaatgga taaatctcat 1409  
 Phe Ser Gly Met Ile Leu Val Lys Phe Val  
 430 435

tgccttttaa cattcaagggt ttttggatt tttt 1443

<210> 30  
 <211> 438  
 <212> PRT  
 <213> Helicobacter pylori

<400> 30  
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 Leu His Ala Ile Glu Met Ile Glu Lys Ala Pro Thr Asn Val Glu Asp  
 20 25 30  
 Arg Asp Lys Ala Pro His Leu Leu Leu Ala Gly Ile Gln Gly Asp  
 35 40 45  
 Glu Pro Gly Gly Phe Asn Ala Thr Asn Leu Phe Leu Met His Tyr Ser  
 50 55 60  
 Val Leu Lys Gly Leu Val Glu Val Val Pro Val Leu Asn Lys Pro Ser  
 65 70 75 80  
 Met Leu Arg Asn His Arg Gly Leu Tyr Gly Asp Met Asn Arg Lys Phe  
 85 90 95  
 Ala Ala Leu Asp Lys Asn Asp Pro Glu Tyr Pro Thr Ile Gln Glu Ile  
 100 105 110  
 Lys Ser Leu Ile Ala Lys Pro Ser Ile Asp Ala Val Leu His Leu His  
 115 120 125  
 Asp Gly Gly Gly Tyr Tyr Arg Pro Val Tyr Val Asp Ala Met Leu Asn  
 130 135 140  
 Pro Lys Arg Trp Gly Asn Cys Phe Ile Ile Asp Gln Asp Glu Val Lys  
 145 150 155 160  
 Gly Ala Lys Phe Pro Asn Leu Leu Ala Phe Ala Asn Asn Thr Ile Glu  
 165 170 175  
 Ser Ile Asn Ala His Leu Leu His Pro Ile Glu Glu Tyr His Leu Lys  
 180 185 190  
 Asn Thr Arg Thr Ala Gln Gly Asp Thr Glu Met Gln Lys Ala Leu Thr  
 195 200 205  
 Phe Tyr Ala Ile Asn Gln Lys Lys Ser Ala Phe Ala Asn Glu Ala Ser  
 210 215 220  
 Lys Glu Leu Pro Leu Ala Ser Arg Val Phe Tyr His Leu Gln Ala Ile  
 225 230 235 240  
 Glu Gly Leu Leu Asn Gln Leu Asn Ile Pro Phe Lys Arg Asp Phe Asp  
 245 250 255  
 Leu Asn Pro Asn Ser Val His Ala Leu Ile Asn Asp Lys Asn Leu Trp  
 260 265 270  
 Ala Lys Ile Ser Ser Leu Pro Lys Met Pro Leu Phe Asn Leu Arg Pro  
 275 280 285  
 Lys Leu Asn His Phe Pro Leu Pro His Asn Thr Lys Ile Pro Gln Ile  
 290 295 300  
 Pro Ile Glu Ser Asn Ala Tyr Ile Val Gly Leu Val Lys Asn Lys Gln  
 305 310 315 320  
 Glu Val Phe Leu Lys Tyr Gly Asn Lys Leu Met Thr Arg Leu Ser Pro  
 325 330 335  
 Phe Tyr Ile Glu Phe Asp Pro Ser Leu Glu Glu Val Lys Met Gln Ile  
 340 345 350  
 Asp Asn Lys Asp Gln Met Val Lys Ile Gly Ser Val Val Glu Val Lys  
 355 360 365

Glu	Ser	Phe	Tyr	Ile	His	Ala	Met	Asp	Asn	Ile	Arg	Ala	Asn	Val	Ile
370						375					380				
Gly	Phe	Ser	Val	Ser	Asn	Glu	Asn	Lys	Pro	Asn	Glu	Ala	Gly	Tyr	Thr
385					390					395					400
Ile	Lys	Phe	Lys	Asp	Phe	Gln	Lys	Arg	Phe	Ser	Leu	Asp	Lys	Gln	Glu
			405					410						415	
Arg	Ile	Tyr	Arg	Ile	Glu	Phe	Tyr	Lys	Asn	Asn	Ala	Phe	Ser	Gly	Met
		420						425					430		
Ile	Leu	Val	Lys	Phe	Val										
		435													

<210> 31  
 <211> 1280  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (66)...(1223)

<400> 31  
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 ttcaa atg tta agg aaa aac att tta gct tac tat ggg gcg aat ttt ctc 110  
 Met Leu Arg Lys Asn Ile Leu Ala Tyr Tyr Gly Ala Asn Phe Leu  
 1 5 10 15

tta atc atc gct caa agc tta ccc cat gcg att tta acc ccc ttg ttg 158  
 Leu Ile Ile Ala Gln Ser Leu Pro His Ala Ile Leu Thr Pro Leu Leu  
 20 25 30

ctt tct aaa ggg ctt agt ttg agt gaa atc ttg ctc gtg caa acc ttt 206  
 Leu Ser Lys Gly Leu Ser Leu Ser Glu Ile Leu Leu Val Gln Thr Phe  
 35 40 45

ttt agc ttt tgc gtg cta gtg gct gaa tac cca agc ggc gtt tta gcg 254  
 Phe Ser Phe Cys Val Leu Val Ala Glu Tyr Pro Ser Gly Val Leu Ala  
 50 55 60

gat ttg atg agc cga aaa aat tta ttc ctg gtt tct aat gcc ttt tta 302  
 Asp Leu Met Ser Arg Lys Asn Leu Phe Leu Val Ser Asn Ala Phe Leu  
 65 70 75

atc gct agt ttt tcg ttt gtg ctg ttt ttt gat agc ttt att ttc atg 350  
 Ile Ala Ser Phe Ser Phe Val Leu Phe Phe Asp Ser Phe Ile Phe Met  
 80 85 90 95

ctt tta gcg tgg ggg ttg tat ggt ttg tat agc gca tgc tct agc ggc 398  
 Leu Leu Ala Trp Gly Leu Tyr Gly Leu Tyr Ser Ala Cys Ser Ser Gly  
 100 105 110

acg att gaa gct tca ctc atc aca gac att aag gaa aac aaa aaa gat 446  
 Thr Ile Glu Ala Ser Leu Ile Thr Asp Ile Lys Glu Asn Lys Lys Asp  
 115 120 125

tta tcc aag ttt tta gcc aaa aac aat caa att act tat tta ggc atg 494  
 Leu Ser Lys Phe Leu Ala Lys Asn Asn Gln Ile Thr Tyr Leu Gly Met  
 130 135 140

att ata ggg agt tct ttg gga tcg ttt ttg tat ctc aaa gtc cat gcg Ile Ile Gly Ser Ser Leu Gly Ser Phe Leu Tyr Leu Lys Val His Ala 145 150 155	542
atg ctg tat att gtg ggg att ttt tta atc atg ctc tgt gtg cta acg Met Leu Tyr Ile Val Gly Ile Phe Leu Ile Met Leu Cys Val Leu Thr 160 165 170 175	590
atc att ttt tat ttt aaa gag aaa gaa ggg gat ttt aaa agc caa aaa Ile Ile Phe Tyr Phe Lys Glu Lys Glu Gly Asp Phe Lys Ser Gln Lys 180 185 190	638
agc ctg aaa ctc ctt aaa gag caa gtc aaa ggc agt ctt aaa gag ctt Ser Leu Lys Leu Leu Lys Glu Gln Val Lys Gly Ser Leu Lys Glu Leu 195 200 205	686
aaa gat aac ccc aaa ctt aaa att ctg tta gtg ggg cat ttg att acg Lys Asp Asn Pro Lys Leu Lys Ile Leu Leu Val Gly His Leu Ile Thr 210 215 220	734
ccc gtc ttt ttt atg agc cat ttt caa atg tgg caa gcg tat ttt tta Pro Val Phe Phe Met Ser His Phe Gln Met Trp Gln Ala Tyr Phe Leu 225 230 235	782
aaa caa ggc gtt aaa gag caa tac ctt ttt gtg ttt tat atc gct ttt Lys Gln Gly Val Lys Glu Gln Tyr Leu Phe Val Phe Tyr Ile Ala Phe 240 245 250 255	830
caa gtg att tct att ctc att cat ttt tta aaa gcc tct agt tat agc Gln Val Ile Ser Ile Leu Ile His Phe Leu Lys Ala Ser Ser Tyr Ser 260 265 270	878
caa aaa atc gcc ttg agt tcg ctt gtg gtg ttg tta ggc gtt agc ccc Gln Lys Ile Ala Leu Ser Ser Leu Val Val Leu Leu Gly Val Ser Pro 275 280 285	926
tta ttg ctt agc aat atc cct tat tgt ttc ata ggg gtg tat gcg ctc Leu Leu Leu Ser Asn Ile Pro Tyr Cys Phe Ile Gly Val Tyr Ala Leu 290 295 300	974
atg gtg gcg ttt ttc act tac atg agc tat tgc tta aac tat caa ttc Met Val Ala Phe Phe Thr Tyr Met Ser Tyr Cys Leu Asn Tyr Gln Phe 305 310 315	1022
tcc aaa ttc gtt tct aaa aac aac att tcc tcg ctc tca tcg ctt tta Ser Lys Phe Val Ser Lys Asn Asn Ile Ser Ser Leu Ser Ser Leu Leu 320 325 330 335	1070
tca agc tgt gtg cgc gtg gtc tct gtg cta atc tta tcg ctc agc agt Ser Ser Cys Val Arg Val Val Ser Val Leu Ile Leu Ser Leu Ser Ser 340 345 350	1118
ctg gaa ctg cgt tac ttc tca ccc cta act atc ata acc atg cat ttt Leu Glu Leu Arg Tyr Phe Ser Pro Leu Thr Ile Ile Thr Met His Phe 355 360 365	1166
gcc ttg acg ctt atc atc ctc ttt ttc ttt ttg tat aag gct aag ccg Ala Leu Thr Leu Ile Ile Leu Phe Phe Phe Leu Tyr Lys Ala Lys Pro 370 375 380	1214

ttt gat gag tgagcggctt taagagtgca accttttagc gatttctata  
Phe Asp Glu  
385

1263

gcaacatcat agccatg

1280

<210> 32  
<211> 386  
<212> PRT  
<213> Helicobacter pylori

<400> 32  
Met Leu Arg Lys Asn Ile Leu Ala Tyr Tyr Gly Ala Asn Phe Leu Leu  
1 5 10 15  
Ile Ile Ala Gln Ser Leu Pro His Ala Ile Leu Thr Pro Leu Leu Leu  
20 25 30  
Ser Lys Gly Leu Ser Leu Ser Glu Ile Leu Leu Val Gln Thr Phe Phe  
35 40 45  
Ser Phe Cys Val Leu Val Ala Glu Tyr Pro Ser Gly Val Leu Ala Asp  
50 55 60  
Leu Met Ser Arg Lys Asn Leu Phe Leu Val Ser Asn Ala Phe Leu Ile  
65 70 75 80  
Ala Ser Phe Ser Phe Val Leu Phe Phe Asp Ser Phe Ile Phe Met Leu  
85 90 95  
Leu Ala Trp Gly Leu Tyr Gly Leu Tyr Ser Ala Cys Ser Ser Gly Thr  
100 105 110  
Ile Glu Ala Ser Leu Ile Thr Asp Ile Lys Glu Asn Lys Lys Asp Leu  
115 120 125  
Ser Lys Phe Leu Ala Lys Asn Asn Gln Ile Thr Tyr Leu Gly Met Ile  
130 135 140  
Ile Gly Ser Ser Leu Gly Ser Phe Leu Tyr Leu Lys Val His Ala Met  
145 150 155 160  
Leu Tyr Ile Val Gly Ile Phe Leu Ile Met Leu Cys Val Leu Thr Ile  
165 170 175  
Ile Phe Tyr Phe Lys Glu Lys Glu Gly Asp Phe Lys Ser Gln Lys Ser  
180 185 190  
Leu Lys Leu Leu Lys Glu Gln Val Lys Gly Ser Leu Lys Glu Leu Lys  
195 200 205  
Asp Asn Pro Lys Leu Lys Ile Leu Leu Val Gly His Leu Ile Thr Pro  
210 215 220  
Val Phe Phe Met Ser His Phe Gln Met Trp Gln Ala Tyr Phe Leu Lys  
225 230 235 240  
Gln Gly Val Lys Glu Gln Tyr Leu Phe Val Phe Tyr Ile Ala Phe Gln  
245 250 255  
Val Ile Ser Ile Leu Ile His Phe Leu Lys Ala Ser Ser Tyr Ser Gln  
260 265 270  
Lys Ile Ala Leu Ser Ser Leu Val Val Leu Leu Gly Val Ser Pro Leu  
275 280 285  
Leu Leu Ser Asn Ile Pro Tyr Cys Phe Ile Gly Val Tyr Ala Leu Met  
290 295 300  
Val Ala Phe Phe Thr Tyr Met Ser Tyr Cys Leu Asn Tyr Gln Phe Ser  
305 310 315 320  
Lys Phe Val Ser Lys Asn Asn Ile Ser Ser Leu Ser Ser Leu Leu Ser  
325 330 335  
Ser Cys Val Arg Val Val Ser Val Leu Ile Leu Ser Leu Ser Ser Leu  
340 345 350  
Glu Leu Arg Tyr Phe Ser Pro Leu Thr Ile Ile Thr Met His Phe Ala  
355 360 365

Leu Thr Leu Ile Ile Leu Phe Phe Phe Leu Tyr Lys Ala Lys Pro Phe  
 370 375 380  
 Asp Glu  
 385

<210> 33  
 <211> 1264  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(1205)

<400> 33  
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 Met Glu  
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 tca gta aaa aca gga aaa aca aat aag gtt ggc aag aat aca gag atg 104  
 Ser Val Lys Thr Gly Lys Thr Asn Lys Val Gly Lys Asn Thr Glu Met  
 5 10 15  
 gct aat aca aag gca aat aaa gag gct cat ttt aaa caa gcg agc acc 152  
 Ala Asn Thr Lys Ala Asn Lys Glu Ala His Phe Lys Gln Ala Ser Thr  
 20 25 30  
 att aca aat ata atc aga tca att cgt ggg att ttt aca aaa att gca 200  
 Ile Thr Asn Ile Ile Arg Ser Ile Arg Gly Ile Phe Thr Lys Ile Ala  
 35 40 45 50  
 aag aaa gtt aga gga ctt gta aaa aaa cac ccc aag aaa agc agt gcg 248  
 Lys Lys Val Arg Gly Leu Val Lys Lys His Pro Lys Lys Ser Ser Ala  
 55 60 65  
 gca tta gta gta ttg acc cat att gcg tgc aag aaa gcg aaa gaa tta 296  
 Ala Leu Val Val Leu Thr His Ile Ala Cys Lys Lys Ala Lys Glu Leu  
 70 75 80  
 gac gat aaa gtc caa gat aaa tcc aaa caa gct gaa aaa gaa aat caa 344  
 Asp Asp Lys Val Gln Asp Lys Ser Lys Gln Ala Glu Lys Glu Asn Gln  
 85 90 95  
 atc aat tgg tgg aaa tat tca gga tta aca ata gcg aca agt tta tta 392  
 Ile Asn Trp Trp Lys Tyr Ser Gly Leu Thr Ile Ala Thr Ser Leu Leu  
 100 105 110  
 tta gcc gct tgt agc act ggt gat gtt agt gaa caa ata gaa cta gaa 440  
 Leu Ala Ala Cys Ser Thr Gly Asp Val Ser Glu Gln Ile Glu Leu Glu  
 115 120 125 130  
 caa gaa aaa caa aag acg agc aat ata gag act aac aat caa ata aaa 488  
 Gln Glu Lys Gln Lys Thr Ser Asn Ile Glu Thr Asn Asn Gln Ile Lys  
 135 140 145  
 gta gaa caa gaa aaa caa aag aca agc aat ata gag act aat aat caa 536  
 Val Glu Gln Glu Lys Gln Lys Thr Ser Asn Ile Glu Thr Asn Asn Gln  
 150 155 160

ata aaa gta gaa caa gaa caa cag aaa aca gaa caa gaa mga cag aaa	584
Ile Lys Val Glu Gln Glu Gln Lys Thr Glu Gln Glu Xaa Gln Lys	
165 170 175	
aca gaa caa gaa aga cag aag aca gaa caa gaa aaa caa aag acc att	632
Thr Glu Gln Glu Arg Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Ile	
180 185 190	
aaa aca cag aaa gat ttc att aaa tat gta gaa caa aat tgc caa gaa	680
Lys Thr Gln Lys Asp Phe Ile Lys Tyr Val Glu Gln Asn Cys Gln Glu	
195 200 205 210	
aat cat aat caa ttc ttt att gaa aaa gga gga att aag gct ggt att	728
Asn His Asn Gln Phe Phe Ile Glu Lys Gly Gly Ile Lys Ala Gly Ile	
215 220 225	
ggt ata gaa gta gaa gct gaa tgc aaa acc cct aaa cct gca aaa acc	776
Gly Ile Glu Val Glu Ala Glu Cys Lys Thr Pro Lys Pro Ala Lys Thr	
230 235 240	
aat caa acc cct atc cag cca aaa cac ctc cca aac tct aaa caa ccc	824
Asn Gln Thr Pro Ile Gln Pro Lys His Leu Pro Asn Ser Lys Gln Pro	
245 250 255	
cgc tct caa aga gga tca aaa gcg caa gag ctt atc gct tat ttg caa	872
Arg Ser Gln Arg Gly Ser Lys Ala Gln Glu Leu Ile Ala Tyr Leu Gln	
260 265 270	
aaa gag cta gaa tct ctg ccc tat tca caa aaa gct atc gct aaa caa	920
Lys Glu Leu Glu Ser Leu Pro Tyr Ser Gln Lys Ala Ile Ala Lys Gln	
275 280 285 290	
gtg gat ttt tat aga cca agt tct atc gct tat tta gaa cta gac cct	968
Val Asp Phe Tyr Arg Pro Ser Ser Ile Ala Tyr Leu Glu Leu Asp Pro	
295 300 305	
aga gat ttt aat gtt aca gaa gaa tgg caa aaa gaa aat tta aaa ata	1016
Arg Asp Phe Asn Val Thr Glu Glu Trp Gln Lys Glu Asn Leu Lys Ile	
310 315 320	
cgc tct aaa gct caa gct aaa atg ctt gaa atg agg agt tta aaa cca	1064
Arg Ser Lys Ala Gln Ala Lys Met Leu Glu Met Arg Ser Leu Lys Pro	
325 330 335	
gac tca caa gcc cac ctt tca acc tct caa agc ctt ttg ttc gtt caa	1112
Asp Ser Gln Ala His Leu Ser Thr Ser Gln Ser Leu Leu Phe Val Gln	
340 345 350	
aaa ata ttt gct gat gtt aat aaa gaa ata aaa gta gtt gct aat act	1160
Lys Ile Phe Ala Asp Val Asn Lys Glu Ile Lys Val Val Ala Asn Thr	
355 360 365 370	
gaa aag aaa gca gaa aaa gcg ggt tat ggt tat agt aaa agg atg	1205
Glu Lys Lys Ala Glu Lys Ala Gly Tyr Gly Tyr Ser Lys Arg Met	
375 380 385	
taggcataag aaaacacccat aaaatcgttc ttagcttatt tatagtattt taaaaactc	1264

<210> 34  
 <211> 385  
 <212> PRT  
 <213> Helicobacter pylori

<400> 34  
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 1 5 10 15  
 Glu Met Ala Asn Thr Lys Ala Asn Lys Glu Ala His Phe Lys Gln Ala  
 20 25 30  
 Ser Thr Ile Thr Asn Ile Ile Arg Ser Ile Arg Gly Ile Phe Thr Lys  
 35 40 45  
 Ile Ala Lys Lys Val Arg Gly Leu Val Lys Lys His Pro Lys Lys Ser  
 50 55 60  
 Ser Ala Ala Leu Val Val Leu Thr His Ile Ala Cys Lys Lys Ala Lys  
 65 70 75 80  
 Glu Leu Asp Asp Lys Val Gln Asp Lys Ser Lys Gln Ala Glu Lys Glu  
 85 90 95  
 Asn Gln Ile Asn Trp Trp Lys Tyr Ser Gly Leu Thr Ile Ala Thr Ser  
 100 105 110  
 Leu Leu Leu Ala Ala Cys Ser Thr Gly Asp Val Ser Glu Gln Ile Glu  
 115 120 125  
 Leu Glu Gln Glu Lys Gln Lys Thr Ser Asn Ile Glu Thr Asn Asn Gln  
 130 135 140  
 Ile Lys Val Glu Gln Glu Lys Gln Lys Thr Ser Asn Ile Glu Thr Asn  
 145 150 155 160  
 Asn Gln Ile Lys Val Glu Gln Glu Gln Lys Thr Glu Gln Glu Xaa  
 165 170 175  
 Gln Lys Thr Glu Gln Glu Arg Gln Lys Thr Glu Gln Glu Lys Gln Lys  
 180 185 190  
 Thr Ile Lys Thr Gln Lys Asp Phe Ile Lys Tyr Val Glu Gln Asn Cys  
 195 200 205  
 Gln Glu Asn His Asn Gln Phe Phe Ile Glu Lys Gly Gly Ile Lys Ala  
 210 215 220  
 Gly Ile Gly Ile Glu Val Glu Ala Glu Cys Lys Thr Pro Lys Pro Ala  
 225 230 235 240  
 Lys Thr Asn Gln Thr Pro Ile Gln Pro Lys His Leu Pro Asn Ser Lys  
 245 250 255  
 Gln Pro Arg Ser Gln Arg Gly Ser Lys Ala Gln Glu Leu Ile Ala Tyr  
 260 265 270  
 Leu Gln Lys Glu Leu Glu Ser Leu Pro Tyr Ser Gln Lys Ala Ile Ala  
 275 280 285  
 Lys Gln Val Asp Phe Tyr Arg Pro Ser Ser Ile Ala Tyr Leu Glu Leu  
 290 295 300  
 Asp Pro Arg Asp Phe Asn Val Thr Glu Glu Trp Gln Lys Glu Asn Leu  
 305 310 315 320  
 Lys Ile Arg Ser Lys Ala Gln Ala Lys Met Leu Glu Met Arg Ser Leu  
 325 330 335  
 Lys Pro Asp Ser Gln Ala His Leu Ser Thr Ser Gln Ser Leu Leu Phe  
 340 345 350  
 Val Gln Lys Ile Phe Ala Asp Val Asn Lys Glu Ile Lys Val Val Ala  
 355 360 365  
 Asn Thr Glu Lys Lys Ala Glu Lys Ala Gly Tyr Gly Tyr Ser Lys Arg  
 370 375 380  
 Met  
 385

<210> 35



<211> 410  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (62)...(340)

<400> 35  
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 t atg aaa aag caa atc ttg aca ggt gtt tta tta tca gtt ttg gca gtg 109  
 Met Lys Lys Gln Ile Leu Thr Gly Val Leu Leu Ser Val Leu Ala Val  
 1 5 10 15  
 agt tct gca tac gct cac aaa gat aaa aaa gac gcc aaa aaa cct aaa 157  
 Ser Ser Ala Tyr Ala His Lys Asp Lys Lys Asp Ala Lys Lys Pro Lys  
 20 25 30  
 ttt agc aca gaa tta gtc gtg gct caa aac gac aaa aaa gac gct aaa 205  
 Phe Ser Thr Glu Leu Val Val Ala Gln Asn Asp Lys Lys Asp Ala Lys  
 35 40 45  
 aaa cct aaa ttt agc aca gaa tta gtc gtg gct caa aac gac aaa aaa 253  
 Lys Pro Lys Phe Ser Thr Glu Leu Val Val Ala Gln Asn Asp Lys Lys  
 50 55 60  
 gac gct aaa aaa cct aaa ttt agc aca gaa tta gtc gtg gct caa aac 301  
 Asp Ala Lys Lys Pro Lys Phe Ser Thr Glu Leu Val Val Ala Gln Asn  
 65 70 75 80  
 gac aaa aaa gac gct aaa aaa cct aaa aac tca gtg gtc taatggcttt 350  
 Asp Lys Lys Asp Ala Lys Lys Pro Lys Asn Ser Val Val  
 85 90  
 gactctaaaa aagcggttttt aaaaacgctt ttttggatat tatectataa tttcctacca 410

<210> 36  
 <211> 93  
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 <213> Helicobacter pylori

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 35 40 45  
 Lys Pro Lys Phe Ser Thr Glu Leu Val Val Ala Gln Asn Asp Lys Lys  
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      Met Ile Tyr Trp Leu Tyr Leu Ala Val Phe Phe Leu Leu Ser
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gca tta gac gct aaa gaa atc gct atg caa cga ttt gac aaa caa aac 156
Ala Leu Asp Ala Lys Glu Ile Ala Met Gln Arg Phe Asp Lys Gln Asn
  15             20             25             30

cat aag att ttt gaa atc ctt gcg gat aaa gtg agc gct aaa gac aat 204
His Lys Ile Phe Glu Ile Leu Ala Asp Lys Val Ser Ala Lys Asp Asn
             35             40             45

gtg ata acc gca tca ggg aat gcg atc tta ttg aat tat gat gtg tat 252
Val Ile Thr Ala Ser Gly Asn Ala Ile Leu Leu Asn Tyr Asp Val Tyr
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att cta gcg gac aag gtg cgt tat gac act aaa acc aaa gaa gcg tta 300
Ile Leu Ala Asp Lys Val Arg Tyr Asp Thr Lys Thr Lys Glu Ala Leu
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tta gag ggg aat atc aag gtt tat agg ggc gag ggt ttg ctc gtt aaa 348
Leu Glu Gly Asn Ile Lys Val Tyr Arg Gly Glu Gly Leu Leu Val Lys
             80             85             90

acc gat tac gtg aaa ttg agt ttg aat gaa aaa tat gaa atc att ttc 396
Thr Asp Tyr Val Lys Leu Ser Leu Asn Glu Lys Tyr Glu Ile Ile Phe
  95             100             105             110

ccc ttt tat gtc caa gac agc gtg agc ggg att tgg gtg agc gcg gat 444
Pro Phe Tyr Val Gln Asp Ser Val Ser Gly Ile Trp Val Ser Ala Asp
             115             120             125

att gcc agc gga aag gat caa aaa tat aag gtt aaa aac atg agc act 492
Ile Ala Ser Gly Lys Asp Gln Lys Tyr Lys Val Lys Asn Met Ser Thr
             130             135             140

tca ggg tgc agc att gat aac ccc att tgg cat gtc aat gcg act tca 540
Ser Gly Cys Ser Ile Asp Asn Pro Ile Trp His Val Asn Ala Thr Ser
             145             150             155

ggc tca ttc aac atg caa aaa tcg cat ttg tct atg tgg aat cct aag 588
Gly Ser Phe Asn Met Gln Lys Ser His Leu Ser Met Trp Asn Pro Lys
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atc tat gtc ggt gat att cct gta ttg tat ttg ccc tat att ttc atg 636
Ile Tyr Val Gly Asp Ile Pro Val Leu Tyr Leu Pro Tyr Ile Phe Met
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tcc acg agc aat aaa aga act act ggg ttt tta tac cct gag ttt ggc 684
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Leu	Ser	Ser	Ser	Arg	Asp	Thr	Leu	Gln	Lys	Tyr	Phe	His	Leu	Lys	Ser					
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gac	tat	gtg	cgt	ttt	gaa	aag	gtt	aat	aag	cgt	atc	aca	gac	gcc	acg	1068				
Asp	Tyr	Val	Arg	Phe	Glu	Lys	Val	Asn	Lys	Arg	Ile	Thr	Asp	Ala	Thr					
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gtg	cgg	gtg	ggc	ttg	caa	ttt	tct	ttg	ttt	aaa	aag	tat	ttg	tct	tta	1356				
Val	Pro	Val	Gly	Leu	Gln	Phe	Ser	Leu	Phe	Lys	Lys	Tyr	Leu	Ser	Leu					
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Arg	Glu	Tyr	Asn	Lys	Leu	Phe	His	Thr	Ile	Gln	Leu	Glu	Ala	Ile	Phe		
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Tyr	Ala	Leu	Ser	Ala	Gln	Ala	Leu	Asn	Ser	Tyr	Thr	Ser	Pro	Leu	Leu		
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Arg	Asp	Tyr	Asp	Tyr	Gln	Gly	Arg	Leu	Tyr	Asp	Ser	Val	Trp	Asn	Pro		
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Ser	Ser	Ile	Leu	Pro	Ser	Asn	Ala	Ser	Asn	Lys	Thr	Val	Asp	Leu	Thr		
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cta	acg	caa	tac	ctt	tat	ggc	tta	ggg	ggg	caa	gag	tta	ttg	tat	ttt	1788	
Leu	Thr	Gln	Tyr	Leu	Tyr	Gly	Leu	Gly	Gly	Gln	Glu	Leu	Leu	Tyr	Phe		
	560					565				570							
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Lys	Ile	Ser	Gln	Leu	Ile	Asn	Leu	Asp	Asp	Lys	Val	Ser	Pro	Phe	Arg		
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atg	cca	cta	gag	agc	aag	atc	ggg	ttt	tcg	ccc	tta	acg	gga	ttg	aac	1884	
Met	Pro	Leu	Glu	Ser	Lys	Ile	Gly	Phe	Ser	Pro	Leu	Thr	Gly	Leu	Asn		
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Ile	Phe	Gly	Asn	Val	Phe	Tyr	Ser	Phe	Tyr	Gln	Asn	Arg	Leu	Glu	Glu		
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Ile	Ser	Val	Asn	Ala	Asn	Tyr	Gln	Arg	Lys	Phe	Leu	Ser	Phe	Asn	Leu		
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Ser	Tyr	Phe	Leu	Lys	Asn	Asn	Phe	Ser	Ser	Gly	Ile	Asn	Ser	Ile	Val		
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gaa	aat	ctg	cgg	att	att	taaaggcggg	ttttagcaac	gacttttggt								2076	
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2097

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 Ile Phe Glu Ile Leu Ala Asp Lys Val Ser Ala Lys Asp Asn Val Ile  
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 Thr Ala Ser Gly Asn Ala Ile Leu Leu Asn Tyr Asp Val Tyr Ile Leu  
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 Ala Asp Lys Val Arg Tyr Asp Thr Lys Thr Lys Glu Ala Leu Leu Glu  
 65 70 75 80  
 Gly Asn Ile Lys Val Tyr Arg Gly Glu Gly Leu Leu Val Lys Thr Asp  
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 Tyr Val Lys Leu Ser Leu Asn Glu Lys Tyr Glu Ile Ile Phe Pro Phe  
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 Tyr Val Gln Asp Ser Val Ser Gly Ile Trp Val Ser Ala Asp Ile Ala  
 115 120 125  
 Ser Gly Lys Asp Gln Lys Tyr Lys Val Lys Asn Met Ser Thr Ser Gly  
 130 135 140  
 Cys Ser Ile Asp Asn Pro Ile Trp His Val Asn Ala Thr Ser Gly Ser  
 145 150 155 160  
 Phe Asn Met Gln Lys Ser His Leu Ser Met Trp Asn Pro Lys Ile Tyr  
 165 170 175  
 Val Gly Asp Ile Pro Val Leu Tyr Leu Pro Tyr Ile Phe Met Ser Thr  
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 Ser Asn Lys Arg Thr Thr Gly Phe Leu Tyr Pro Glu Phe Gly Thr Ser  
 195 200 205  
 Asn Leu Asp Gly Phe Ile Tyr Leu Gln Pro Phe Tyr Leu Ala Pro Lys  
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 225 230 235 240  
 Phe Gly Leu Asn Phe Glu Ala Arg Tyr Ile Asn Ser Lys Asn Asp Arg  
 245 250 255  
 Phe Leu Phe Asn Ala Arg Tyr Phe Arg Asn Tyr Thr Gln Tyr Val Lys  
 260 265 270  
 Arg Tyr Asp Leu Arg Asn Gln Asn Ile Tyr Gly Phe Glu Phe Leu Ser  
 275 280 285  
 Ser Ser Arg Asp Thr Leu Gln Lys Tyr Phe His Leu Lys Ser Asn Ile  
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 Asp Asn Gly His Tyr Ile Asp Phe Leu Tyr Met Asn Asp Leu Asp Tyr  
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 Val Arg Phe Glu Lys Val Asn Lys Arg Ile Thr Asp Ala Thr His Met  
 325 330 335  
 Ser Arg Ala Asn Tyr Tyr Leu Gln Thr Glu Asn Asn Tyr Tyr Gly Leu  
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 Phe Gln Ser Val Pro Asn Leu Gln Tyr His Lys Tyr Leu Asn Ser Leu  
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 Tyr Phe Arg Asn Leu Leu Tyr Ser Val Asp Tyr Gln Phe Arg Asn Thr  
 385 390 395 400  
 Ala Arg Glu Ile Gly Tyr Gly Tyr Val Gln Asn Ala Leu Asn Val Pro



agt aat gag tct tta ttt ggc gct aaa ggg cct gca agc ttt atg gcg 320  
 Ser Asn Glu Ser Leu Phe Gly Ala Lys Gly Pro Ala Ser Phe Met Ala  
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 aaa tta acc atg ttt tta ggg ctg tta ttt gtc atc aac acc atc gct 368  
 Lys Leu Thr Met Phe Leu Gly Leu Leu Phe Val Ile Asn Thr Ile Ala  
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 Leu Gly Tyr Phe Tyr Asn Lys Glu Tyr Gly Lys Ser Val Leu Asp Glu  
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 act aaa acc aac aaa gaa ctt tcg ccc cta gtc cct gcc acc ggc acg 464  
 Thr Lys Thr Asn Lys Glu Leu Ser Pro Leu Val Pro Ala Thr Gly Thr  
 85 90 95  
 ctt aac cct gca ctt aat ccc aca tta aac cca acg ctc aac cct tta 512  
 Leu Asn Pro Ala Leu Asn Pro Thr Leu Asn Pro Thr Leu Asn Pro Leu  
 100 105 110 115  
 gag caa gcc cca act aat cct tta atg cca caa caa acg cct aac gaa 560  
 Glu Gln Ala Pro Thr Asn Pro Leu Met Pro Gln Gln Thr Pro Asn Glu  
 120 125 130  
 ctc cct aaa gag cca gcc aaa acg cct tct gtt gaa agc ccc aaa cag 608  
 Leu Pro Lys Glu Pro Ala Lys Thr Pro Ser Val Glu Ser Pro Lys Gln  
 135 140 145  
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 Asn Glu Lys Asn Glu Lys Asn Asp Ala Lys Glu Asn Gly Ile Lys Gly  
 150 155 160  
 gtt gaa aaa acc aaa gag aac gcc aaa acg ccc cca acc acc cac caa 704  
 Val Glu Lys Thr Lys Glu Asn Ala Lys Thr Pro Pro Thr Thr His Gln  
 165 170 175  
 aag cct aaa acg cat gca acg caa acc aac gcc cat acc aac caa aaa 752  
 Lys Pro Lys Thr His Ala Thr Gln Thr Asn Ala His Thr Asn Gln Lys  
 180 185 190 195  
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 Lys Asp Glu Lys

gcaaaaaagc attcaagctt taaacaggga tttttccact ctaaggagcg cgaaagtttc 864  
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 Tyr Ser Gly Ser Asn Glu Ser Leu Phe Gly Ala Lys Gly Pro Ala Ser





Leu	Leu	Lys	Glu	Ile	Glu	Arg	Ser	Ile	Gln	Glu	Ala	Asn	Ile	Gly	Val		
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Asn	Pro	Asn	Asn	Asp	Gly	Glu	Thr	Ile	Lys	Leu	Phe	Phe	Pro	Pro	Met		
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Thr	Ser	Glu	Gln	Arg	Lys	Leu	Ile	Ala	Lys	Asp	Ala	Lys	Ala	Met	Gly		
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gaa	aag	gct	aaa	gtg	gct	gtg	agg	aat	atc	cgc	caa	gat	gct	aac	aac	735	
Glu	Lys	Ala	Lys	Val	Ala	Val	Arg	Asn	Ile	Arg	Gln	Asp	Ala	Asn	Asn		
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Gln	Val	Lys	Lys	Leu	Glu	Lys	Asp	Lys	Glu	Ile	Ser	Glu	Asp	Glu	Ser		
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aaa	aaa	gcc	caa	gag	cag	atc	caa	aaa	atc	acc	gat	gaa	gcc	att	aaa	831	
Lys	Lys	Ala	Gln	Glu	Gln	Ile	Gln	Lys	Ile	Thr	Asp	Glu	Ala	Ile	Lys		
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170					175				180					185			
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Ser	Val	Asn	Ile	Leu	Asp	His	Ile	Lys	Val	Asp	Tyr	Tyr	Gly	Thr	Pro		
		35				40					45						
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Ser	Ile	Gln	Glu	Ala	Asn	Ile	Gly	Val	Asn	Pro	Asn	Asn	Asp	Gly	Glu		
			85						90					95			
Thr	Ile	Lys	Leu	Phe	Phe	Pro	Pro	Met	Thr	Ser	Glu	Gln	Arg	Lys	Leu		
		100						105					110				
Ile	Ala	Lys	Asp	Ala	Lys	Ala	Met	Gly	Glu	Lys	Ala	Lys	Val	Ala	Val		
		115					120					125					
Arg	Asn	Ile	Arg	Gln	Asp	Ala	Asn	Asn	Gln	Val	Lys	Lys	Leu	Glu	Lys		
	130				135						140						
Asp	Lys	Glu	Ile	Ser	Glu	Asp	Glu	Ser	Lys	Lys	Ala	Gln	Glu	Gln	Ile		
145				150					155					160			
Gln	Lys	Ile	Thr	Asp	Glu	Ala	Ile	Lys	Lys	Ile	Asp	Glu	Ser	Val	Lys		
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 tgcacaaaat cgccccact atcttaaaaa agaggctata aa atg gct caa aat 174  
 Met Ala Gln Asn  
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ttc acg aaa ctc aac ccc cag ttt gaa aac atc att ttt gaa cat gac 222  
 Phe Thr Lys Leu Asn Pro Gln Phe Glu Asn Ile Ile Phe Glu His Asp  
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gac aac caa atg att tta aac ttt ggc ccc caa cac ccc agt agt cat 270  
 Asp Asn Gln Met Ile Leu Asn Phe Gly Pro Gln His Pro Ser Ser His  
 25 30 35

ggg caa ttg cgc ttg att ttg gaa tta gag ggc gaa aaa atc att aag 318  
 Gly Gln Leu Arg Leu Ile Leu Glu Leu Glu Gly Glu Lys Ile Ile Lys  
 40 45 50

gct acc cct gaa att ggc tac ttg cat aga ggc tgt gaa aag tta ggc 366  
 Ala Thr Pro Glu Ile Gly Tyr Leu His Arg Gly Cys Glu Lys Leu Gly  
 55 60 65

gaa aac atg acc tat aac gaa tac atg ccc act act gat aga ttg gat 414  
 Glu Asn Met Thr Tyr Asn Glu Tyr Met Pro Thr Thr Asp Arg Leu Asp  
 70 75 80

tac act tct tct acc agc aat aat tac gct tac gct tat gcg gta gag 462  
 Tyr Thr Ser Ser Thr Ser Asn Asn Tyr Ala Tyr Ala Tyr Ala Val Glu  
 85 90 95 100

acc tta ctc aat tta gaa atc cca cgc cga gcg cag gtg atc cgc acg 510  
 Thr Leu Leu Asn Leu Glu Ile Pro Arg Arg Ala Gln Val Ile Arg Thr  
 105 110 115

att tta cta gag ctt aac cgc atg atc tca cac atc ttt ttt atc agc 558  
 Ile Leu Leu Glu Leu Asn Arg Met Ile Ser His Ile Phe Phe Ile Ser  
 120 125 130

gtg cat gct tta gat gtg ggg gcg atg agc gtg ttt ttg tat gcg ttt 606  
 Val His Ala Leu Asp Val Gly Ala Met Ser Val Phe Leu Tyr Ala Phe  
 135 140 145

aaa acg agg gaa tac ggc ttg gat ttg atg gag gat tat tgc ggg gct 654  
 Lys Thr Arg Glu Tyr Gly Leu Asp Leu Met Glu Asp Tyr Cys Gly Ala  
 150 155 160

agg ctc acg cat aac gct ata agg att ggg ggc gtg cct tta gat tta	702
Arg Leu Thr His Asn Ala Ile Arg Ile Gly Gly Val Pro Leu Asp Leu	
165 170 175 180	
ccc cct aat tgg tta gaa ggc tta aaa aag ttt tta ggc gaa atg agg	750
Pro Pro Asn Trp Leu Glu Gly Leu Lys Lys Phe Leu Gly Glu Met Arg	
185 190 195	
gaa tgc aaa aaa ctc att caa ggc tta ttg gat aag aat cgc att tgg	798
Glu Cys Lys Lys Leu Ile Gln Gly Leu Leu Asp Lys Asn Arg Ile Trp	
200 205 210	
cgg atg cgc ttg gaa aat gtg ggc gtt gta acg caa aaa atg gcg caa	846
Arg Met Arg Leu Glu Asn Val Gly Val Val Thr Gln Lys Met Ala Gln	
215 220 225	
agc tgg ggc atg agc ggt atc atg tta aga ggg act ggg atc gct tat	894
Ser Trp Gly Met Ser Gly Ile Met Leu Arg Gly Thr Gly Ile Ala Tyr	
230 235 240	
gac atc aga aaa gaa gag cct tat gag ctt tat aaa gag ctt gat ttt	942
Asp Ile Arg Lys Glu Glu Pro Tyr Glu Leu Tyr Lys Glu Leu Asp Phe	
245 250 255 260	
gat gtg ccg gtg ggc aat tat ggc gat agt tat gat agg tat tgt ttg	990
Asp Val Pro Val Gly Asn Tyr Gly Asp Ser Tyr Asp Arg Tyr Cys Leu	
265 270 275	
tat atg tta gaa att gat gaa agc gtt cgc atc att gaa cag ctc att	1038
Tyr Met Leu Glu Ile Asp Glu Ser Val Arg Ile Ile Glu Gln Leu Ile	
280 285 290	
cct atg tat gct aaa acc gat acg cct atc atg gct caa aac ccg cat	1086
Pro Met Tyr Ala Lys Thr Asp Thr Pro Ile Met Ala Gln Asn Pro His	
295 300 305	
tat att tcc gcc cct aaa gaa gat ata atg acg caa aac tac gcc ttg	1134
Tyr Ile Ser Ala Pro Lys Glu Asp Ile Met Thr Gln Asn Tyr Ala Leu	
310 315 320	
atg cag cat ttt gtt tta gtg gct cag ggc atg cgt ccg ccc gtt ggg	1182
Met Gln His Phe Val Leu Val Ala Gln Gly Met Arg Pro Pro Val Gly	
325 330 335 340	
gaa gtg tat gcc ccc aca gaa agc cct aaa ggg gaa tta ggg ttt ttt	1230
Glu Val Tyr Ala Pro Thr Glu Ser Pro Lys Gly Glu Leu Gly Phe Phe	
345 350 355	
atc cat tca gag ggc gag cct tac cct cac agg cta aaa atc aga gcc	1278
Ile His Ser Glu Gly Glu Pro Tyr Pro His Arg Leu Lys Ile Arg Ala	
360 365 370	
cct agc ttt tat cac att ggg gct ttg agc gac att tta gtg ggg caa	1326
Pro Ser Phe Tyr His Ile Gly Ala Leu Ser Asp Ile Leu Val Gly Gln	
375 380 385	
tat tta gcg gat gca gta acc gtg att ggc tca acc aat gcg gtg ttt	1374
Tyr Leu Ala Asp Ala Val Thr Val Ile Gly Ser Thr Asn Ala Val Phe	

390

395

400

ggc gag gtg gat aga tgaaacgctt tgatttacgc cccttaaaag cgggtatttt 1429  
 Gly Glu Val Asp Arg  
 405

tgaacgctta gaagaattga ttgaaaaaga aatgcaacct aatgaagtcg ctattttcat 1489  
 gtttgaagtg ggggattttt ctaatatccc taagagcgct gaatttatcc aatctaaagg 1549  
 gcatgagctc ctcaattctt tgcgtttcaa tcaagcggat tggacgattg tcgtgagaaa 1609  
 aaaggcttga ttttgagcgg cttaacccc ttaaattctc ccttagtcgc aagctcttct 1669

&lt;210&gt; 44

&lt;211&gt; 409

&lt;212&gt; PRT

<213> *Helicobacter pylori*

&lt;400&gt; 44

Met	Ala	Gln	Asn	Phe	Thr	Lys	Leu	Asn	Pro	Gln	Phe	Glu	Asn	Ile	Ile
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Phe	Glu	His	Asp	Asp	Asn	Gln	Met	Ile	Leu	Asn	Phe	Gly	Pro	Gln	His
		20					25					30			
Pro	Ser	Ser	His	Gly	Gln	Leu	Arg	Leu	Ile	Leu	Glu	Leu	Glu	Gly	Glu
	35					40					45				
Lys	Ile	Ile	Lys	Ala	Thr	Pro	Glu	Ile	Gly	Tyr	Leu	His	Arg	Gly	Cys
50					55				60						
Glu	Lys	Leu	Gly	Glu	Asn	Met	Thr	Tyr	Asn	Glu	Tyr	Met	Pro	Thr	Thr
65				70				75						80	
Asp	Arg	Leu	Asp	Tyr	Thr	Ser	Ser	Thr	Ser	Asn	Asn	Tyr	Ala	Tyr	Ala
			85					90					95		
Tyr	Ala	Val	Glu	Thr	Leu	Leu	Asn	Leu	Glu	Ile	Pro	Arg	Arg	Ala	Gln
		100					105					110			
Val	Ile	Arg	Thr	Ile	Leu	Leu	Glu	Leu	Asn	Arg	Met	Ile	Ser	His	Ile
	115					120					125				
Phe	Phe	Ile	Ser	Val	His	Ala	Leu	Asp	Val	Gly	Ala	Met	Ser	Val	Phe
	130					135				140					
Leu	Tyr	Ala	Phe	Lys	Thr	Arg	Glu	Tyr	Gly	Leu	Asp	Leu	Met	Glu	Asp
145				150				155						160	
Tyr	Cys	Gly	Ala	Arg	Leu	Thr	His	Asn	Ala	Ile	Arg	Ile	Gly	Gly	Val
			165					170					175		
Pro	Leu	Asp	Leu	Pro	Pro	Asn	Trp	Leu	Glu	Gly	Leu	Lys	Lys	Phe	Leu
		180				185						190			
Gly	Glu	Met	Arg	Glu	Cys	Lys	Lys	Leu	Ile	Gln	Gly	Leu	Leu	Asp	Lys
	195					200					205				
Asn	Arg	Ile	Trp	Arg	Met	Arg	Leu	Glu	Asn	Val	Gly	Val	Val	Thr	Gln
	210				215					220					
Lys	Met	Ala	Gln	Ser	Trp	Gly	Met	Ser	Gly	Ile	Met	Leu	Arg	Gly	Thr
225				230				235						240	
Gly	Ile	Ala	Tyr	Asp	Ile	Arg	Lys	Glu	Glu	Pro	Tyr	Glu	Leu	Tyr	Lys
			245					250					255		
Glu	Leu	Asp	Phe	Asp	Val	Pro	Val	Gly	Asn	Tyr	Gly	Asp	Ser	Tyr	Asp
		260					265					270			
Arg	Tyr	Cys	Leu	Tyr	Met	Leu	Glu	Ile	Asp	Glu	Ser	Val	Arg	Ile	Ile
	275					280					285				
Glu	Gln	Leu	Ile	Pro	Met	Tyr	Ala	Lys	Thr	Asp	Thr	Pro	Ile	Met	Ala
	290				295					300					
Gln	Asn	Pro	His	Tyr	Ile	Ser	Ala	Pro	Lys	Glu	Asp	Ile	Met	Thr	Gln
305				310					315					320	
Asn	Tyr	Ala	Leu	Met	Gln	His	Phe	Val	Leu	Val	Ala	Gln	Gly	Met	Arg

				325					330					335					
Pro	Pro	Val	Gly	Glu	Val	Tyr	Ala	Pro	Thr	Glu	Ser	Pro	Lys	Gly	Glu				
			340					345					350						
Leu	Gly	Phe	Phe	Ile	His	Ser	Glu	Gly	Glu	Pro	Tyr	Pro	His	Arg	Leu				
		355					360					365							
Lys	Ile	Arg	Ala	Pro	Ser	Phe	Tyr	His	Ile	Gly	Ala	Leu	Ser	Asp	Ile				
	370					375					380								
Leu	Val	Gly	Gln	Tyr	Leu	Ala	Asp	Ala	Val	Thr	Val	Ile	Gly	Ser	Thr				
385					390				395						400				
Asn	Ala	Val	Phe	Gly	Glu	Val	Asp	Arg											
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 <212> DNA  
 <213> Helicobacter pylori

<220>  
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 <222> (358)...(732)

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 ccaatattgg ctatcattta ctttgatttc gcccatcgtg tcatgttcaa ttctaaattg 180  
 catgctaata ctttgaaatt tgatttttaa accttaaaaa aatagcataa actcttatac 240  
 cttctactta aaaaccctaa ttttttaaac accattttcca caattttttac acaaaagagg 300  
 gttattatcc gttcgcaaca agaattttct tgttatctta atgtaaaggc caaaacg atg 360  
 Met  
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aaa	aag	tta	gcc	gct	tta	ttt	tta	gta	agc	gtg	ttg	ggg	gtt	atg	ggt	408
Lys	Lys	Leu	Ala	Ala	Leu	Phe	Leu	Val	Ser	Val	Leu	Gly	Val	Met	Gly	
		5						10					15			

tta	aac	gca	tgg	gag	caa	acc	cta	aaa	gct	aat	gac	ttg	gaa	gtg	aaa	456
Leu	Asn	Ala	Trp	Glu	Gln	Thr	Leu	Lys	Ala	Asn	Asp	Leu	Glu	Val	Lys	
	20					25					30					

atc	aaa	tcc	gtg	ggt	aac	ccc	att	aaa	ggc	gat	aac	act	ttc	att	ctc	504
Ile	Lys	Ser	Val	Gly	Asn	Pro	Ile	Lys	Gly	Asp	Asn	Thr	Phe	Ile	Leu	
	35				40					45						

agc	ccc	act	tta	aaa	ggt	aag	gct	tta	gaa	aaa	gct	atc	gtt	agg	gtg	552
Ser	Pro	Thr	Leu	Lys	Gly	Lys	Ala	Leu	Glu	Lys	Ala	Ile	Val	Arg	Val	
	50				55				60					65		

cag	ttt	atg	atg	cct	gaa	atg	ccc	ggc	atg	cca	gcg	atg	aaa	gaa	atg	600
Gln	Phe	Met	Met	Pro	Glu	Met	Pro	Gly	Met	Pro	Ala	Met	Lys	Glu	Met	
			70					75						80		

gcg	caa	gtg	agt	gaa	aaa	aac	ggc	ctt	tat	gaa	gct	aaa	acc	aat	ctt	648
Ala	Gln	Val	Ser	Glu	Lys	Asn	Gly	Leu	Tyr	Glu	Ala	Lys	Thr	Asn	Leu	
		85					90						95			

tct	atg	aac	ggg	aca	tgg	cag	gtt	agg	gtg	gat	att	aaa	tct	aaa	gag	696
Ser	Met	Asn	Gly	Thr	Trp	Gln	Val	Arg	Val	Asp	Ile	Lys	Ser	Lys	Glu	
		100				105						110				

ggt cag gtt tat cgc gct aaa aca agc ctg gat tta taagagcatg 742  
 Gly Gln Val Tyr Arg Ala Lys Thr Ser Leu Asp Leu  
 115 120 125

ctatcttttta taagcgcggtt tgataaaagg ggcgtttcaa tacgcctttt aacagccttg 802  
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 taccttt 869

<210> 46  
 <211> 125  
 <212> PRT  
 <213> Helicobacter pylori

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 Gly Leu Asn Ala Trp Glu Gln Thr Leu Lys Ala Asn Asp Leu Glu Val  
 20 25 30  
 Lys Ile Lys Ser Val Gly Asn Pro Ile Lys Gly Asp Asn Thr Phe Ile  
 35 40 45  
 Leu Ser Pro Thr Leu Lys Gly Lys Ala Leu Glu Lys Ala Ile Val Arg  
 50 55 60  
 Val Gln Phe Met Met Pro Glu Met Pro Gly Met Pro Ala Met Lys Glu  
 65 70 75 80  
 Met Ala Gln Val Ser Glu Lys Asn Gly Leu Tyr Glu Ala Lys Thr Asn  
 85 90 95  
 Leu Ser Met Asn Gly Thr Trp Gln Val Arg Val Asp Ile Lys Ser Lys  
 100 105 110  
 Glu Gly Gln Val Tyr Arg Ala Lys Thr Ser Leu Asp Leu  
 115 120 125

<210> 47  
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 <212> DNA  
 <213> Helicobacter pylori

<220>  
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 <222> (73)...(1152)

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 aaaaagggtgg tt atg aat ggt ttt tgc gct aga cta cga gcc ata act cat 111  
 Met Asn Gly Phe Cys Ala Arg Leu Arg Ala Ile Thr His  
 1 5 10

aat gaa aga tta aaa atg aaa ata gcg gta tta ctc agt ggg ggg gtg 159  
 Asn Glu Arg Leu Lys Met Lys Ile Ala Val Leu Leu Ser Gly Gly Val  
 15 20 25

gat agc tct tat agc gct tat agc tta aaa gag caa ggg cat gaa tta 207  
 Asp Ser Ser Tyr Ser Ala Tyr Ser Leu Lys Glu Gln Gly His Glu Leu  
 30 35 40 45

gtg ggg att tat tta aaa ctc cat gcg agt gaa aaa aag cat gat tta 255  
 Val Gly Ile Tyr Leu Lys Leu His Ala Ser Glu Lys Lys His Asp Leu  
 50 55 60

tac atc aaa aac gct caa aaa gca tgc gag ttt tta ggc att cct tta	303
Tyr Ile Lys Asn Ala Gln Lys Ala Cys Glu Phe Leu Gly Ile Pro Leu	
65 70 75	
gag gtg ttg gat ttt caa aag gat ttt aaa agc gcg gtt tat gat gaa	351
Glu Val Leu Asp Phe Gln Lys Asp Phe Lys Ser Ala Val Tyr Asp Glu	
80 85 90	
ttt atc aac gcc tat gaa gaa ggg caa acc cca aac cct tgt gcg ttg	399
Phe Ile Asn Ala Tyr Glu Glu Gly Gln Thr Pro Asn Pro Cys Ala Leu	
95 100 105	
tgc aac cct tta atg aag ttt ggg cta gct ttg gat cac gct tta aaa	447
Cys Asn Pro Leu Met Lys Phe Gly Leu Ala Leu Asp His Ala Leu Lys	
110 115 120 125	
tta ggg tgt gaa aag atc gct acc ggg cat tat gcg aga gtc aaa gaa	495
Leu Gly Cys Glu Lys Ile Ala Thr Gly His Tyr Ala Arg Val Lys Glu	
130 135 140	
att gac aaa ata agt tat att caa gag gct ttg gat aaa act aaa gat	543
Ile Asp Lys Ile Ser Tyr Ile Gln Glu Ala Leu Asp Lys Thr Lys Asp	
145 150 155	
cag agc tat ttt tta tac gct tta gag cat gaa gtg atc gct aaa ttg	591
Gln Ser Tyr Phe Leu Tyr Ala Leu Glu His Glu Val Ile Ala Lys Leu	
160 165 170	
gtg ttc cct tta ggg gat ttg cta aaa aag gat att aag cct tta gcc	639
Val Phe Pro Leu Gly Asp Leu Leu Lys Lys Asp Ile Lys Pro Leu Ala	
175 180 185	
ttg aat gcg atg cct ttt tta ggc act tta gag act tat aag gaa tct	687
Leu Asn Ala Met Pro Phe Leu Gly Thr Leu Glu Thr Tyr Lys Glu Ser	
190 195 200 205	
caa gaa atc tgc ttt gtg gaa aaa agc tac att gac act tta aaa aag	735
Gln Glu Ile Cys Phe Val Glu Lys Ser Tyr Ile Asp Thr Leu Lys Lys	
210 215 220	
cat gtt gaa gtg gaa aaa gag ggc gtg gtg aaa aac cta caa ggc gaa	783
His Val Glu Val Glu Lys Glu Gly Val Val Lys Asn Leu Gln Gly Glu	
225 230 235	
gtc att ggc acg cat aaa ggc tat atg caa tac acg att ggc aaa cgc	831
Val Ile Gly Thr His Lys Gly Tyr Met Gln Tyr Thr Ile Gly Lys Arg	
240 245 250	
aaa ggc ttt agt att aaa ggc gcg tta gag ccg cat ttt gtg gtg ggg	879
Lys Gly Phe Ser Ile Lys Gly Ala Leu Glu Pro His Phe Val Val Gly	
255 260 265	
att gac gct aaa aag aac gag cta gtc gtg ggc aaa aaa gaa gat ctc	927
Ile Asp Ala Lys Lys Asn Glu Leu Val Val Gly Lys Lys Glu Asp Leu	
270 275 280 285	
gcc acg cat tcg ctt aag gct aaa aac aaa tct tta atg aaa gat ttt	975
Ala Thr His Ser Leu Lys Ala Lys Asn Lys Ser Leu Met Lys Asp Phe	

290										295					300					
aaa	gat	ggc	gaa	tat	ttt	atc	aag	gct	cgt	tac	agg	agc	gtg	cct	gct	1023				
Lys	Asp	Gly	Glu	Tyr	Phe	Ile	Lys	Ala	Arg	Tyr	Arg	Ser	Val	Pro	Ala					
		305						310					315							
aaa	gcg	cat	gtg	agt	ttg	aaa	gat	gag	gtg	att	gaa	gtg	ggg	ttt	aaa	1071				
Lys	Ala	His	Val	Ser	Leu	Lys	Asp	Glu	Val	Ile	Glu	Val	Gly	Phe	Lys					
		320					325					330								
gag	cct	ttt	tat	ggc	gtg	gct	aaa	ggg	caa	gct	ttg	gtc	ggt	tat	aaa	1119				
Glu	Pro	Phe	Tyr	Gly	Val	Ala	Lys	Gly	Gln	Ala	Leu	Val	Val	Tyr	Lys					
	335					340					345									
gat	gac	atc	ttg	ctt	ggg	ggg	ggc	gtg	att	gtt	taaaaaactaa	agaactaaga	1172							
Asp	Asp	Ile	Leu	Leu	Gly	Gly	Gly	Val	Ile	Val										
350				355				360												
gatacgcctt ttggcagtct cttaatgttt tattgaatag gcgtt 1217																				
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<212> PRT																				
<213> Helicobacter pylori																				
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Leu	Lys	Met	Lys	Ile	Ala	Val	Leu	Leu	Ser	Gly	Gly	Val	Asp	Ser	Ser					
		20						25					30							
Tyr	Ser	Ala	Tyr	Ser	Leu	Lys	Glu	Gln	Gly	His	Glu	Leu	Val	Gly	Ile					
	35					40					45									
Tyr	Leu	Lys	Leu	His	Ala	Ser	Glu	Lys	Lys	His	Asp	Leu	Tyr	Ile	Lys					
	50				55					60										
Asn	Ala	Gln	Lys	Ala	Cys	Glu	Phe	Leu	Gly	Ile	Pro	Leu	Glu	Val	Leu					
65				70					75					80						
Asp	Phe	Gln	Lys	Asp	Phe	Lys	Ser	Ala	Val	Tyr	Asp	Glu	Phe	Ile	Asn					
		85						90					95							
Ala	Tyr	Glu	Glu	Gln	Thr	Pro	Asn	Pro	Cys	Ala	Leu	Cys	Asn	Pro						
		100					105					110								
Leu	Met	Lys	Phe	Gly	Leu	Ala	Leu	Asp	His	Ala	Leu	Lys	Leu	Gly	Cys					
	115					120					125									
Glu	Lys	Ile	Ala	Thr	Gly	His	Tyr	Ala	Arg	Val	Lys	Glu	Ile	Asp	Lys					
	130				135					140										
Ile	Ser	Tyr	Ile	Gln	Glu	Ala	Leu	Asp	Lys	Thr	Lys	Asp	Gln	Ser	Tyr					
145				150					155					160						
Phe	Leu	Tyr	Ala	Leu	Glu	His	Glu	Val	Ile	Ala	Lys	Leu	Val	Phe	Pro					
		165					170						175							
Leu	Gly	Asp	Leu	Leu	Lys	Lys	Asp	Ile	Lys	Pro	Leu	Ala	Leu	Asn	Ala					
		180					185					190								
Met	Pro	Phe	Leu	Gly	Thr	Leu	Glu	Thr	Tyr	Lys	Glu	Ser	Gln	Glu	Ile					
	195					200						205								
Cys	Phe	Val	Glu	Lys	Ser	Tyr	Ile	Asp	Thr	Leu	Lys	Lys	His	Val	Glu					
	210				215						220									
Val	Glu	Lys	Glu	Gly	Val	Val	Lys	Asn	Leu	Gln	Gly	Glu	Val	Ile	Gly					
225				230					235					240						
Thr	His	Lys	Gly	Tyr	Met	Gln	Tyr	Thr	Ile	Gly	Lys	Arg	Lys	Gly	Phe					
			245					250						255						
Ser	Ile	Lys	Gly	Ala	Leu	Glu	Pro	His	Phe	Val	Val	Gly	Ile	Asp	Ala					



			260					265				270					
Lys	Lys	Asn	Glu	Leu	Val	Val	Gly	Lys	Lys	Glu	Asp	Leu	Ala	Thr	His		
		275					280					285					
Ser	Leu	Lys	Ala	Lys	Asn	Lys	Ser	Leu	Met	Lys	Asp	Phe	Lys	Asp	Gly		
	290					295					300						
Glu	Tyr	Phe	Ile	Lys	Ala	Arg	Tyr	Arg	Ser	Val	Pro	Ala	Lys	Ala	His		
305					310					315					320		
Val	Ser	Leu	Lys	Asp	Glu	Val	Ile	Glu	Val	Gly	Phe	Lys	Glu	Pro	Phe		
			325					330						335			
Tyr	Gly	Val	Ala	Lys	Gly	Gln	Ala	Leu	Val	Val	Tyr	Lys	Asp	Asp	Ile		
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Leu	Leu	Gly	Gly	Gly	Val	Ile	Val										
	355						360										

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 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (191)...(793)

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 ttgtctattc gcatgcgttt atttaccct attctttaag tttttatcca taacttataa 120  
 gggtttttagt tttagcatgt tagcattcag ccaccactct ttttaaggaa tttgtttgaa 180  
 gtttcaaatt atg agt ttg tta gcc act ctt tta tta gcc tct tgc ttg 229  
 Met Ser Leu Leu Ala Thr Leu Leu Leu Ala Ser Cys Leu  
 1 5 10

ccc ccc aaa ggc cat cat tct ggt ttg gtg aat ctt tat atc gct cat 277  
 Pro Pro Lys Gly His His Ser Gly Leu Val Asn Leu Tyr Ile Ala His  
 15 20 25

caa ggc caa agc gtg cgc act tat tgg cgc aaa gtg gat aga gga gtt 325  
 Gln Gly Gln Ser Val Arg Thr Tyr Trp Arg Lys Val Asp Arg Gly Val  
 30 35 40 45

atc gct aaa cac aat gaa gcg ctt aaa aaa gat cct aaa gca aag ctc 373  
 Ile Ala Lys His Asn Glu Ala Leu Lys Lys Asp Pro Lys Ala Lys Leu  
 50 55 60

aaa gac ccc agg ggg cct tta ttc atg cta ggg agt gag cgc ttc atg 421  
 Lys Asp Pro Arg Gly Pro Leu Phe Met Leu Gly Ser Glu Arg Phe Met  
 65 70 75

ctt tta tgg aaa aac cgc tac gct tta gcc aag ccc caa tcg ttc agg 469  
 Leu Leu Trp Lys Asn Arg Tyr Ala Leu Ala Lys Pro Gln Ser Phe Arg  
 80 85 90

cta gag cct ggt ttt tat tac ttg gat tct ttt agc gtg gaa act caa 517  
 Leu Glu Pro Gly Phe Tyr Tyr Leu Asp Ser Phe Ser Val Glu Thr Gln  
 95 100 105

aaa ggc gtc ttg cag agc gct cct ggc tat tca tat act aaa aat ggc 565  
 Lys Gly Val Leu Gln Ser Ala Pro Gly Tyr Ser Tyr Thr Lys Asn Gly  
 110 115 120 125

tat gat ttc aaa aac aac cgc ccc ttt ttc ctg gcc ttt gaa gtc aaa	613
Tyr Asp Phe Lys Asn Asn Arg Pro Phe Phe Leu Ala Phe Glu Val Lys	
130 135 140	

cct gat ggc aaa acc att ctt cct agc gtg gaa tta agc ctg att aaa	661
Pro Asp Gly Lys Thr Ile Leu Pro Ser Val Glu Leu Ser Leu Ile Lys	
145 150 155	

acc cct aga ggc ttt tta ggg gtg ttc ttg ttt gat aat aat gaa aag	709
Thr Pro Arg Gly Phe Leu Gly Val Phe Leu Phe Asp Asn Asn Glu Lys	
160 165 170	

ggg act aac gcc aag tgg att gag ggg agt ttg aat tta aag ctt aaa	757
Gly Thr Asn Ala Lys Trp Ile Glu Gly Ser Leu Asn Leu Lys Leu Lys	
175 180 185	

aac gct tcc ttt aaa gat gcg tgg ggg ttg gaa caa taaagcatga	803
Asn Ala Ser Phe Lys Asp Ala Trp Gly Leu Glu Gln	
190 195 200	

agtgatcgct tgcttttcgt aagctcttta tgattagatt gtaaaaaaat gccttgagta	863
tttttttagat tttattaccc ctattcaatt ggaacaaagc cattaaattt ttaaaaactt	923
ttaaaaacga taaacataat ccgcgctcca agtaacatag ctttcaaaaa tg	975

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 <212> PRT  
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Ser Val Arg Thr Tyr Trp Arg Lys Val Asp Arg Gly Val Ile Ala Lys	
35 40 45	
His Asn Glu Ala Leu Lys Lys Asp Pro Lys Ala Lys Leu Lys Asp Pro	
50 55 60	
Arg Gly Pro Leu Phe Met Leu Gly Ser Glu Arg Phe Met Leu Leu Trp	
65 70 75 80	
Lys Asn Arg Tyr Ala Leu Ala Lys Pro Gln Ser Phe Arg Leu Glu Pro	
85 90 95	
Gly Phe Tyr Tyr Leu Asp Ser Phe Ser Val Glu Thr Gln Lys Gly Val	
100 105 110	
Leu Gln Ser Ala Pro Gly Tyr Ser Tyr Thr Lys Asn Gly Tyr Asp Phe	
115 120 125	
Lys Asn Asn Arg Pro Phe Phe Leu Ala Phe Glu Val Lys Pro Asp Gly	
130 135 140	
Lys Thr Ile Leu Pro Ser Val Glu Leu Ser Leu Ile Lys Thr Pro Arg	
145 150 155 160	
Gly Phe Leu Gly Val Phe Leu Phe Asp Asn Asn Glu Lys Gly Thr Asn	
165 170 175	
Ala Lys Trp Ile Glu Gly Ser Leu Asn Leu Lys Leu Lys Asn Ala Ser	
180 185 190	
Phe Lys Asp Ala Trp Gly Leu Glu Gln	
195 200	

<210> 51  
 <211> 1116  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (90)...(1076)

<400> 51  
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 tatgaatttg tttattaagg gaaaaaatc atg tca aat agc atg ttg gat aaa 113  
 Met Ser Asn Ser Met Leu Asp Lys  
 1 5

aat aaa gcg att ctt aca ggg ggt ggg gct tta tta tta ggg cta atc 161  
 Asn Lys Ala Ile Leu Thr Gly Gly Gly Ala Leu Leu Leu Gly Leu Ile  
 10 15 20

gtg ctt ttt tat tta gct tat cgc cct aag gct gaa gtg ttg caa ggg 209  
 Val Leu Phe Tyr Leu Ala Tyr Arg Pro Lys Ala Glu Val Leu Gln Gly  
 25 30 35 40

ttt ttg gaa gcc aga gaa tac agc gtg agc tcc aaa gtc cct ggc cgc 257  
 Phe Leu Glu Ala Arg Glu Tyr Ser Val Ser Ser Lys Val Pro Gly Arg  
 45 50 55

att gaa aag gtg ttt gtt aaa aaa ggc gat cac att aaa aag ggc gat 305  
 Ile Glu Lys Val Phe Val Lys Lys Gly Asp His Ile Lys Lys Gly Asp  
 60 65 70

ttg gtt ttt agc att tct agc cct gaa tta gaa gcc aaa ctc gct caa 353  
 Leu Val Phe Ser Ile Ser Ser Pro Glu Leu Glu Ala Lys Leu Ala Gln  
 75 80 85

gct gaa gcc ggg cat aaa gcc gct aaa gcg ctt agc gat gaa gtc aaa 401  
 Ala Glu Ala Gly His Lys Ala Ala Lys Ala Leu Ser Asp Glu Val Lys  
 90 95 100

aga ggc tca aga gac gaa acg att aat tct gcg aga gac gtt tgg caa 449  
 Arg Gly Ser Arg Asp Glu Thr Ile Asn Ser Ala Arg Asp Val Trp Gln  
 105 110 115 120

gca gcc aaa tcc caa gcc act tta gcc aaa gag act tat aag cgc gtt 497  
 Ala Ala Lys Ser Gln Ala Thr Leu Ala Lys Glu Thr Tyr Lys Arg Val  
 125 130 135

caa gat ttg tat gat aat ggc gtg gcg agc ttg caa aag cgc gat gaa 545  
 Gln Asp Leu Tyr Asp Asn Gly Val Ala Ser Leu Gln Lys Arg Asp Glu  
 140 145 150

gcc tat gcg gct tat gaa agc act aaa tac aac gag agc gcg gct tac 593  
 Ala Tyr Ala Ala Tyr Glu Ser Thr Lys Tyr Asn Glu Ser Ala Ala Tyr  
 155 160 165

caa aag tat aaa atg gct tta ggg ggg gcg agc tct gaa agt aag att 641  
 Gln Lys Tyr Lys Met Ala Leu Gly Gly Ala Ser Ser Glu Ser Lys Ile  
 170 175 180

gcc gct aag gct aaa gag agc gcg gct tta ggg caa gtg aat gaa gtg 689  
 Ala Ala Lys Ala Lys Glu Ser Ala Ala Leu Gly Gln Val Asn Glu Val  
 185 190 195 200  
 gag tct tat tta aaa gac gtc aaa gcg aca gcc cca att gat ggg gaa 737  
 Glu Ser Tyr Leu Lys Asp Val Lys Ala Thr Ala Pro Ile Asp Gly Glu  
 205 210 215  
 gtg agt aac gtg ctt tta agc ggt ggc gag ctt agc cct aag ggt ttt 785  
 Val Ser Asn Val Leu Leu Ser Gly Gly Glu Leu Ser Pro Lys Gly Phe  
 220 225 230  
 cct gtg gtt tta atg ata gat tta aag gat agt tgg tta aaa atc agc 833  
 Pro Val Val Leu Met Ile Asp Leu Lys Asp Ser Trp Leu Lys Ile Ser  
 235 240 245  
 gtg cct gaa aag tat ttg aac gag ttt aaa gtg ggt aag gaa ttt gaa 881  
 Val Pro Glu Lys Tyr Leu Asn Glu Phe Lys Val Gly Lys Glu Phe Glu  
 250 255 260  
 ggc tat atc ccg gcg ttg aaa aaa agc acg aaa ttc agg gtc aaa tat 929  
 Gly Tyr Ile Pro Ala Leu Lys Lys Ser Thr Lys Phe Arg Val Lys Tyr  
 265 270 275 280  
 ttg agc gtg atg ggg gat ttt gcg act tgg aaa gcg acg aat aat tcc 977  
 Leu Ser Val Met Gly Asp Phe Ala Thr Trp Lys Ala Thr Asn Asn Ser  
 285 290 295  
 aac act tac gac atg aaa agc tat gaa gtg gaa gcc ata ccc tta gaa 1025  
 Asn Thr Tyr Asp Met Lys Ser Tyr Glu Val Glu Ala Ile Pro Leu Glu  
 300 305 310  
 gag ttg gaa aat ttt agg gta ggg atg agc gtg tta gtt acc att aaa 1073  
 Glu Leu Glu Asn Phe Arg Val Gly Met Ser Val Leu Val Thr Ile Lys  
 315 320 325  
 cct taataaggat tgttttgttc agattgataa gcgcattgggt 1116  
 Pro

<210> 52  
 <211> 329  
 <212> PRT  
 <213> *Helicobacter pylori*

<400> 52  
 Met Ser Asn Ser Met Leu Asp Lys Asn Lys Ala Ile Leu Thr Gly Gly  
 1 5 10 15  
 Gly Ala Leu Leu Gly Leu Ile Val Leu Phe Tyr Leu Ala Tyr Arg  
 20 25 30  
 Pro Lys Ala Glu Val Leu Gln Gly Phe Leu Glu Ala Arg Glu Tyr Ser  
 35 40 45  
 Val Ser Ser Lys Val Pro Gly Arg Ile Glu Lys Val Phe Val Lys Lys  
 50 55 60  
 Gly Asp His Ile Lys Lys Gly Asp Leu Val Phe Ser Ile Ser Ser Pro  
 65 70 75 80  
 Glu Leu Glu Ala Lys Leu Ala Gln Ala Glu Ala Gly His Lys Ala Ala  
 85 90 95

Lys	Ala	Leu	Ser	Asp	Glu	Val	Lys	Arg	Gly	Ser	Arg	Asp	Glu	Thr	Ile	
			100					105					110			
Asn	Ser	Ala	Arg	Asp	Val	Trp	Gln	Ala	Ala	Lys	Ser	Gln	Ala	Thr	Leu	
			115					120					125			
Ala	Lys	Glu	Thr	Tyr	Lys	Arg	Val	Gln	Asp	Leu	Tyr	Asp	Asn	Gly	Val	
			130			135					140					
Ala	Ser	Leu	Gln	Lys	Arg	Asp	Glu	Ala	Tyr	Ala	Tyr	Glu	Ser	Thr		
145					150				155					160		
Lys	Tyr	Asn	Glu	Ser	Ala	Ala	Tyr	Gln	Lys	Tyr	Lys	Met	Ala	Leu	Gly	
			165						170					175		
Gly	Ala	Ser	Ser	Glu	Ser	Lys	Ile	Ala	Ala	Lys	Ala	Lys	Glu	Ser	Ala	
			180					185					190			
Ala	Leu	Gly	Gln	Val	Asn	Glu	Val	Glu	Ser	Tyr	Leu	Lys	Asp	Val	Lys	
		195				200						205				
Ala	Thr	Ala	Pro	Ile	Asp	Gly	Glu	Val	Ser	Asn	Val	Leu	Leu	Ser	Gly	
		210				215					220					
Gly	Glu	Leu	Ser	Pro	Lys	Gly	Phe	Pro	Val	Val	Leu	Met	Ile	Asp	Leu	
225					230					235					240	
Lys	Asp	Ser	Trp	Leu	Lys	Ile	Ser	Val	Pro	Glu	Lys	Tyr	Leu	Asn	Glu	
			245						250					255		
Phe	Lys	Val	Gly	Lys	Glu	Phe	Glu	Gly	Tyr	Ile	Pro	Ala	Leu	Lys	Lys	
			260					265					270			
Ser	Thr	Lys	Phe	Arg	Val	Lys	Tyr	Leu	Ser	Val	Met	Gly	Asp	Phe	Ala	
		275					280					285				
Thr	Trp	Lys	Ala	Thr	Asn	Asn	Ser	Asn	Thr	Tyr	Asp	Met	Lys	Ser	Tyr	
		290				295					300					
Glu	Val	Glu	Ala	Ile	Pro	Leu	Glu	Glu	Leu	Glu	Asn	Phe	Arg	Val	Gly	
305					310					315					320	
Met	Ser	Val	Leu	Val	Thr	Ile	Lys	Pro								
				325												

<210> 53  
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 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (94)...(1467)

<400> 53  
 aaataaaata gcgatcatta taacatgttg ctttttaagt gaaagcggtta agttgttagg 60  
 gtatagtggc ttaaaaattt taggatattg aga atg ctt gaa act tct agc cat 114  
 Met Leu Glu Thr Ser Ser His  
 1 5

ttt tta aaa tcg ttt cgc ttg aag cgt tat ata ggg ttt tta ttg att 162  
 Phe Leu Lys Ser Phe Arg Leu Lys Arg Tyr Ile Gly Phe Leu Leu Ile  
 10 15 20

tct tta gcg tta tta atc acg ccc ttt gtt cgc att gat ggg gcg cat 210  
 Ser Leu Ala Leu Leu Ile Thr Pro Phe Val Arg Ile Asp Gly Ala His  
 25 30 35

ttg ttt ttg atc tct ttt gag cat aag caa ctg cat ttt tta ggc aag 258  
 Leu Phe Leu Ile Ser Phe Glu His Lys Gln Leu His Phe Leu Gly Lys  
 40 45 50 55

atc ttt agc gct gaa gaa ttg caa gtc atg cct ttt atg gtt att ttg Ile Phe Ser Ala Glu Glu Leu Gln Val Met Pro Phe Met Val Ile Leu 60 65 70	306
ctt ttt ata ggg att ttt ttc atc acc act agc ctt ggg cgt gtg tgg Leu Phe Ile Gly Ile Phe Phe Ile Thr Thr Ser Leu Gly Arg Val Trp 75 80 85	354
tgc ggt tgg gct tgc ccg caa acc ttt tta agg gtg ctt tat aga gat Cys Gly Trp Ala Cys Pro Gln Thr Phe Leu Arg Val Leu Tyr Arg Asp 90 95 100	402
gtg att gaa acc aag att ttc aaa ctc cat aaa aag atc agc aac aag Val Ile Glu Thr Lys Ile Phe Lys Leu His Lys Lys Ile Ser Asn Lys 105 110 115	450
caa gaa agc cct aaa aac acc cca agc tac aag atc cgt aaa gta ttg Gln Glu Ser Pro Lys Asn Thr Pro Ser Tyr Lys Ile Arg Lys Val Leu 120 125 130 135	498
agc gtt tta ttg ttc gct cct gtt gtg gcg ggg cta atg atg ttg ttt Ser Val Leu Leu Phe Ala Pro Val Val Ala Gly Leu Met Met Leu Phe 140 145 150	546
ttc ttt tat ttc atc gcc cca gaa gat ttt ttt atg tat ctt aaa aac Phe Phe Tyr Phe Ile Ala Pro Glu Asp Phe Phe Met Tyr Leu Lys Asn 155 160 165	594
cct agc gat cac cct att gct atg ggt ttt tgg ctt ttt agc acg gct Pro Ser Asp His Pro Ile Ala Met Gly Phe Trp Leu Phe Ser Thr Ala 170 175 180	642
gtg gtg cta ttt gat ata gtg gtg gtt gcg gag cgt ttt tgc att tat Val Val Leu Phe Asp Ile Val Val Val Ala Glu Arg Phe Cys Ile Tyr 185 190 195	690
tta tgc cct tac gct agg gtg caa tcg gtg ttg tat gac aat gac acc Leu Cys Pro Tyr Ala Arg Val Gln Ser Val Leu Tyr Asp Asn Asp Thr 200 205 210 215	738
tta aac cct att tat gat gaa aag cgc ggc gga gcg ctt tat aat aat Leu Asn Pro Ile Tyr Asp Glu Lys Arg Gly Gly Ala Leu Tyr Asn Asn 220 225 230	786
cag ggc cat ctc ttc ccc tta cct ccc aaa aaa cgc agc cca gaa aac Gln Gly His Leu Phe Pro Leu Pro Pro Lys Lys Arg Ser Pro Glu Asn 235 240 245	834
gaa tgc gtg aat tgt ttg cat tgc gtg cag gtt tgc ccc acg cat att Glu Cys Val Asn Cys Leu His Cys Val Gln Val Cys Pro Thr His Ile 250 255 260	882
gac atc agg aag ggc ttg caa tta gaa tgc atc aat tgt tta gaa tgc Asp Ile Arg Lys Gly Leu Gln Leu Glu Cys Ile Asn Cys Leu Glu Cys 265 270 275	930
gtg gat gca tgc acg att acc atg gct aaa ttt aac cgc cct tca ctc Val Asp Ala Cys Thr Ile Thr Met Ala Lys Phe Asn Arg Pro Ser Leu 280 285 290 295	978

atc caa tgg tct tca act aac gct att aat acg cgc caa aaa gtg cac 1026  
 Ile Gln Trp Ser Ser Thr Asn Ala Ile Asn Thr Arg Gln Lys Val His  
 300 305 310  
 ctg gtg cgt tta aaa acg atc gct tac atg ggg gtt atc gct att gtg 1074  
 Leu Val Arg Leu Lys Thr Ile Ala Tyr Met Gly Val Ile Ala Ile Val  
 315 320 325  
 atc gct ctt tta gcc atc act tcg ttt aaa aaa gaa cgc atg ctc tta 1122  
 Ile Ala Leu Leu Ala Ile Thr Ser Phe Lys Lys Glu Arg Met Leu Leu  
 330 335 340  
 gac att aac cgc aac agc gat ctg tat gaa ttg cgc tct agc ggg tat 1170  
 Asp Ile Asn Arg Asn Ser Asp Leu Tyr Glu Leu Arg Ser Ser Gly Tyr  
 345 350 355  
 gtg gat aac gat tac gtg ttt tta ttc cac aac acg gac aat aaa gac 1218  
 Val Asp Asn Asp Tyr Val Phe Leu Phe His Asn Thr Asp Asn Lys Asp  
 360 365 370 375  
 cat gag ttt tat ttc aaa gtt tta ggg caa aaa gac att cag atc aaa 1266  
 His Glu Phe Tyr Phe Lys Val Leu Gly Gln Lys Asp Ile Gln Ile Lys  
 380 385 390  
 aag cct tta aat cct atc gcc att aaa gcc ggg caa aag att aaa gcg 1314  
 Lys Pro Leu Asn Pro Ile Ala Ile Lys Ala Gly Gln Lys Ile Lys Ala  
 395 400 405  
 gta gtg att tta aga aaa ccc cta aag agt aac gcc aca gaa tac aag 1362  
 Val Val Ile Leu Arg Lys Pro Leu Lys Ser Asn Ala Thr Glu Tyr Lys  
 410 415 420  
 aac gct aaa gac gct cta atc ccc att acc ata caa gct tat agc gcg 1410  
 Asn Ala Lys Asp Ala Leu Ile Pro Ile Thr Ile Gln Ala Tyr Ser Ala  
 425 430 435  
 gac gat aag aat att acg ata gaa agg gaa tcg gtg ttt att gca cca 1458  
 Asp Asp Lys Asn Ile Thr Ile Glu Arg Glu Ser Val Phe Ile Ala Pro  
 440 445 450 455  
 agt gag gat tgaagcctaa aactagcggt caatcacttc ataaggcaag 1507  
 Ser Glu Asp  
 ccttggtt 1514

<210> 54  
 <211> 458  
 <212> PRT  
 <213> Helicobacter pylori

<400> 54  
 Met Leu Glu Thr Ser Ser His Phe Leu Lys Ser Phe Arg Leu Lys Arg  
 1 5 10 15  
 Tyr Ile Gly Phe Leu Leu Ile Ser Leu Ala Leu Leu Ile Thr Pro Phe  
 20 25 30  
 Val Arg Ile Asp Gly Ala His Leu Phe Leu Ile Ser Phe Glu His Lys  
 35 40 45

Gln	Leu	His	Phe	Leu	Gly	Lys	Ile	Phe	Ser	Ala	Glu	Glu	Leu	Gln	Val
50						55					60				
Met	Pro	Phe	Met	Val	Ile	Leu	Leu	Phe	Ile	Gly	Ile	Phe	Phe	Ile	Thr
65					70					75					80
Thr	Ser	Leu	Gly	Arg	Val	Trp	Cys	Gly	Trp	Ala	Cys	Pro	Gln	Thr	Phe
				85					90					95	
Leu	Arg	Val	Leu	Tyr	Arg	Asp	Val	Ile	Glu	Thr	Lys	Ile	Phe	Lys	Leu
			100					105					110		
His	Lys	Lys	Ile	Ser	Asn	Lys	Gln	Glu	Ser	Pro	Lys	Asn	Thr	Pro	Ser
		115					120					125			
Tyr	Lys	Ile	Arg	Lys	Val	Leu	Ser	Val	Leu	Leu	Phe	Ala	Pro	Val	Val
		130				135					140				
Ala	Gly	Leu	Met	Met	Leu	Phe	Phe	Phe	Tyr	Phe	Ile	Ala	Pro	Glu	Asp
145					150					155					160
Phe	Phe	Met	Tyr	Leu	Lys	Asn	Pro	Ser	Asp	His	Pro	Ile	Ala	Met	Gly
				165					170					175	
Phe	Trp	Leu	Phe	Ser	Thr	Ala	Val	Val	Leu	Phe	Asp	Ile	Val	Val	Val
			180					185					190		
Ala	Glu	Arg	Phe	Cys	Ile	Tyr	Leu	Cys	Pro	Tyr	Ala	Arg	Val	Gln	Ser
		195					200					205			
Val	Leu	Tyr	Asp	Asn	Asp	Thr	Leu	Asn	Pro	Ile	Tyr	Asp	Glu	Lys	Arg
		210				215						220			
Gly	Gly	Ala	Leu	Tyr	Asn	Asn	Gln	Gly	His	Leu	Phe	Pro	Leu	Pro	Pro
225					230					235					240
Lys	Lys	Arg	Ser	Pro	Glu	Asn	Glu	Cys	Val	Asn	Cys	Leu	His	Cys	Val
				245					250					255	
Gln	Val	Cys	Pro	Thr	His	Ile	Asp	Ile	Arg	Lys	Gly	Leu	Gln	Leu	Glu
			260					265					270		
Cys	Ile	Asn	Cys	Leu	Glu	Cys	Val	Asp	Ala	Cys	Thr	Ile	Thr	Met	Ala
		275					280					285			
Lys	Phe	Asn	Arg	Pro	Ser	Leu	Ile	Gln	Trp	Ser	Ser	Thr	Asn	Ala	Ile
		290				295					300				
Asn	Thr	Arg	Gln	Lys	Val	His	Leu	Val	Arg	Leu	Lys	Thr	Ile	Ala	Tyr
305					310					315					320
Met	Gly	Val	Ile	Ala	Ile	Val	Ile	Ala	Leu	Leu	Ala	Ile	Thr	Ser	Phe
				325					330					335	
Lys	Lys	Glu	Arg	Met	Leu	Leu	Asp	Ile	Asn	Arg	Asn	Ser	Asp	Leu	Tyr
			340					345					350		
Glu	Leu	Arg	Ser	Ser	Gly	Tyr	Val	Asp	Asn	Asp	Tyr	Val	Phe	Leu	Phe
		355					360					365			
His	Asn	Thr	Asp	Asn	Lys	Asp	His	Glu	Phe	Tyr	Phe	Lys	Val	Leu	Gly
		370				375					380				
Gln	Lys	Asp	Ile	Gln	Ile	Lys	Lys	Pro	Leu	Asn	Pro	Ile	Ala	Ile	Lys
385					390					395					400
Ala	Gly	Gln	Lys	Ile	Lys	Ala	Val	Val	Ile	Leu	Arg	Lys	Pro	Leu	Lys
				405					410					415	
Ser	Asn	Ala	Thr	Glu	Tyr	Lys	Asn	Ala	Lys	Asp	Ala	Leu	Ile	Pro	Ile
			420					425					430		
Thr	Ile	Gln	Ala	Tyr	Ser	Ala	Asp	Lys	Asn	Ile	Thr	Ile	Glu	Arg	
		435					440				445				
Glu	Ser	Val	Phe	Ile	Ala	Pro	Ser	Glu	Asp						
450						455									

<210> 55  
 <211> 990  
 <212> DNA  
 <213> Helicobacter pylori



<220>  
 <221> CDS  
 <222> (228)...(782)

<400> 55  
 acgatttgat caataacgaa aataaaattg atgaaatcaa taatgaagaa aacgctgac 60  
 cttcgcaaaa aagaacgaac aacgttttgc aacgagccac taaccaccaa gacaatctca 120  
 attccccact caacaggaag tattaaagtg tgaaactttt ttcaaaggat ttatttataa 180  
 aagtaacccc tttattttta agcgttttatt ttttaaacc caccatt atg caa gcc 236  
 Met Gln Ala  
 1

aaa agc cgt ttt tat gtg gct tct caa tac cag gtg ggg aaa atg atc 284  
 Lys Ser Arg Phe Tyr Val Ala Ser Gln Tyr Gln Val Gly Lys Met Ile  
 5 10 15

atg aaa aaa tac aac gat ctc aaa cgc acg att gaa ggg gcg agc ttt 332  
 Met Lys Lys Tyr Asn Asp Leu Lys Arg Thr Ile Glu Gly Ala Ser Phe  
 20 25 30 35

tct tta ggc tgg gag att aac ccc act aac tac tgg ttt tat tcg cgc 380  
 Ser Leu Gly Trp Glu Ile Asn Pro Thr Asn Tyr Trp Phe Tyr Ser Arg  
 40 45 50

tat tac ttt ttt atg gat tac ggg aat gtc att ctc aat aaa aga acg 428  
 Tyr Tyr Phe Phe Met Asp Tyr Gly Asn Val Ile Leu Asn Lys Arg Thr  
 55 60 65

ggc gct caa gcg aac atg ttc act tat ggc ttt ggg ggg gat ttg att 476  
 Gly Ala Gln Ala Asn Met Phe Thr Tyr Gly Phe Gly Gly Asp Leu Ile  
 70 75 80

gtg gaa tac aat aaa aac ccc ttg tat gta ttt tct ctt ttt tat ggc 524  
 Val Glu Tyr Asn Lys Asn Pro Leu Tyr Val Phe Ser Leu Phe Tyr Gly  
 85 90 95

atg caa gtt gct gaa aac aca tgg acg att tcc aaa cac agc gcg aat 572  
 Met Gln Val Ala Glu Asn Thr Trp Thr Ile Ser Lys His Ser Ala Asn  
 100 105 110 115

ttc atc att gac gat tgg cgc agc att caa ggg ttt tcg ctc aaa act 620  
 Phe Ile Ile Asp Asp Trp Arg Ser Ile Gln Gly Phe Ser Leu Lys Thr  
 120 125 130

tcc aat ttt agg atg ttg ggt tta gtg ggg ttt aaa ttc caa acc gtg 668  
 Ser Asn Phe Arg Met Leu Gly Leu Val Gly Phe Lys Phe Gln Thr Val  
 135 140 145

cta ttc cac cat gac gca agt att gaa gtg ggg atc aaa tgg cct ttt 716  
 Leu Phe His His Asp Ala Ser Ile Glu Val Gly Ile Lys Trp Pro Phe  
 150 155 160

gct ttt gaa tac gac tca gcc ttt gta agg ctt ttt tct gtc ttt att 764  
 Ala Phe Glu Tyr Asp Ser Ala Phe Val Arg Leu Phe Ser Val Phe Ile  
 165 170 175

tcg cac act ttc tac ctt taaactaatt ccaaccctac cgggcaatga 812  
 Ser His Thr Phe Tyr Leu  
 180 185

tcgctcccta aaatatcttt atagattaaa gcgtctttta agcgcgtttt taaaggggta 872  
gagcataaaa aataatcaat gcgccaacca atgtttttat cccttgcttg ttgcatgtaa 932  
ctccaccagg tgtaagcctt ttcttttgta gggtaaaaaat aacggaaagt gtcaataa 990

<210> 56  
<211> 185  
<212> PRT  
<213> Helicobacter pylori

<400> 56  
Met Gln Ala Lys Ser Arg Phe Tyr Val Ala Ser Gln Tyr Gln Val Gly  
1 5 10 15  
Lys Met Ile Met Lys Lys Tyr Asn Asp Leu Lys Arg Thr Ile Glu Gly  
20 25 30  
Ala Ser Phe Ser Leu Gly Trp Glu Ile Asn Pro Thr Asn Tyr Trp Phe  
35 40 45  
Tyr Ser Arg Tyr Tyr Phe Phe Met Asp Tyr Gly Asn Val Ile Leu Asn  
50 55 60  
Lys Arg Thr Gly Ala Gln Ala Asn Met Phe Thr Tyr Gly Phe Gly Gly  
65 70 75 80  
Asp Leu Ile Val Glu Tyr Asn Lys Asn Pro Leu Tyr Val Phe Ser Leu  
85 90 95  
Phe Tyr Gly Met Gln Val Ala Glu Asn Thr Trp Thr Ile Ser Lys His  
100 105 110  
Ser Ala Asn Phe Ile Ile Asp Asp Trp Arg Ser Ile Gln Gly Phe Ser  
115 120 125  
Leu Lys Thr Ser Asn Phe Arg Met Leu Gly Leu Val Gly Phe Lys Phe  
130 135 140  
Gln Thr Val Leu Phe His His Asp Ala Ser Ile Glu Val Gly Ile Lys  
145 150 155 160  
Trp Pro Phe Ala Phe Glu Tyr Asp Ser Ala Phe Val Arg Leu Phe Ser  
165 170 175  
Val Phe Ile Ser His Thr Phe Tyr Leu  
180 185

<210> 57  
<211> 1161  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (109)...(1113)

<400> 57  
atcttacctt tatcttttaa gattttatga aaaatagttt catttttact attgttat 60  
tcttagtaat gttataatcg ctttataaat catacaaaaa ggatcgct atg tta gtt 117  
Met Leu Val  
1  
act cgc ttt aaa aaa gct ttc att tct tat tct tta ggc gtg ctt gtc 165  
Thr Arg Phe Lys Lys Ala Phe Ile Ser Tyr Ser Leu Gly Val Leu Val  
5 10 15  
gct tca tta tgg ttg aac gtg tgc aac gct tca gcg caa gaa gtc aaa 213  
Ala Ser Leu Trp Leu Asn Val Cys Asn Ala Ser Ala Gln Glu Val Lys  
20 25 30 35

gtc aag gat tat ttc ggg gag caa acc atc aag ctt cct gtt tct aaa	261
Val Lys Asp Tyr Phe Gly Glu Gln Thr Ile Lys Leu Pro Val Ser Lys	
40 45 50	
ata gcc tat ata ggg agc tat gta gaa gtg cct gcc atg ctt aat gtt	309
Ile Ala Tyr Ile Gly Ser Tyr Val Glu Val Pro Ala Met Leu Asn Val	
55 60 65	
tgg aat agg gtt gta ggc gtt tcg gat tac gct ttt aaa gac gat att	357
Trp Asn Arg Val Val Gly Val Ser Asp Tyr Ala Phe Lys Asp Asp Ile	
70 75 80	
gtc aaa gcc act ctc aaa ggc gaa gat ctt aaa cgc gtc aaa cac atg	405
Val Lys Ala Thr Leu Lys Gly Glu Asp Leu Lys Arg Val Lys His Met	
85 90 95	
agc act gat cat aca gcc gcg cta aat gta gag ctt tta aaa aag ctt	453
Ser Thr Asp His Thr Ala Ala Leu Asn Val Glu Leu Leu Lys Lys Leu	
100 105 110 115	
agc cct gat ctt gtg gta acc ttt gtg ggc aac cct aaa gcg gta gag	501
Ser Pro Asp Leu Val Val Thr Phe Val Gly Asn Pro Lys Ala Val Glu	
120 125 130	
cat gcg aaa aaa ttt ggt ata tca ttt ctt tct ttt caa gag aca acg	549
His Ala Lys Lys Phe Gly Ile Ser Phe Leu Ser Phe Gln Glu Thr Thr	
135 140 145	
att gca gag gcc atg cag gcc atg caa gct caa gcc acg gtt tta gag	597
Ile Ala Glu Ala Met Gln Ala Met Gln Ala Gln Ala Thr Val Leu Glu	
150 155 160	
att gac gct tcc aaa aaa ttc gcc aaa atg caa gaa act ttg gat ttt	645
Ile Asp Ala Ser Lys Lys Phe Ala Lys Met Gln Glu Thr Leu Asp Phe	
165 170 175	
att gct gag cgt ttg aaa aat gtc aaa aag aaa aag ggg gtg gag ctt	693
Ile Ala Glu Arg Leu Lys Asn Val Lys Lys Lys Lys Gly Val Glu Leu	
180 185 190 195	
ttc cat aaa gcc aat aaa atc agc ggc cat caa gcc att agc tca gac	741
Phe His Lys Ala Asn Lys Ile Ser Gly His Gln Ala Ile Ser Ser Asp	
200 205 210	
att tta gaa aaa ggg ggc ata gac aat ttt ggc ttg aaa tat gtc aaa	789
Ile Leu Glu Lys Gly Gly Ile Asp Asn Phe Gly Leu Lys Tyr Val Lys	
215 220 225	
ttt ggg cgt gct gac att agc gtg gaa aaa atc gtt aaa gaa aac cct	837
Phe Gly Arg Ala Asp Ile Ser Val Glu Lys Ile Val Lys Glu Asn Pro	
230 235 240	
gag att atc ttt att tgg tgg ata agc cca ctc acg cct gaa gat gtg	885
Glu Ile Ile Phe Ile Trp Trp Ile Ser Pro Leu Thr Pro Glu Asp Val	
245 250 255	
tta aac aac ccc aaa ttt gct acc atc aaa gcc att aaa aac aag cag	933
Leu Asn Asn Pro Lys Phe Ala Thr Ile Lys Ala Ile Lys Asn Lys Gln	

260	265	270	275	
ggt tat aaa ctc ccc aca atg gat att ggc ggg cct aga gcc cca ctc				981
Val Tyr Lys Leu Pro Thr Met Asp Ile Gly Gly Pro Arg Ala Pro Leu				
	280	285	290	
ata agt ctt ttt atc gct cta aaa gcc cac cct gaa gcc ttt aag ggc				1029
Ile Ser Leu Phe Ile Ala Leu Lys Ala His Pro Glu Ala Phe Lys Gly				
	295	300	305	
gtg gat att aat gcg atg gtt aaa gac tac tat aaa gtg gtt ttt gat				1077
Val Asp Ile Asn Ala Met Val Lys Asp Tyr Tyr Lys Val Val Phe Asp				
	310	315	320	
ttg aat gat gca gag gtt gag ccc ttt tta tgg cat taatttttaa				1123
Leu Asn Asp Ala Glu Val Glu Pro Phe Leu Trp His				
	325	330	335	
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Val Leu Val Ala Ser Leu Trp Leu Asn Val Cys Asn Ala Ser Ala Gln				
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Glu Val Lys Val Lys Asp Tyr Phe Gly Glu Gln Thr Ile Lys Leu Pro				
	35	40	45	
Val Ser Lys Ile Ala Tyr Ile Gly Ser Tyr Val Glu Val Pro Ala Met				
	50	55	60	
Leu Asn Val Trp Asn Arg Val Val Gly Val Ser Asp Tyr Ala Phe Lys				
	65	70	75	80
Asp Asp Ile Val Lys Ala Thr Leu Lys Gly Glu Asp Leu Lys Arg Val				
	85	90	95	
Lys His Met Ser Thr Asp His Thr Ala Leu Asn Val Glu Leu Leu				
	100	105	110	
Lys Lys Leu Ser Pro Asp Leu Val Thr Phe Val Gly Asn Pro Lys				
	115	120	125	
Ala Val Glu His Ala Lys Lys Phe Gly Ile Ser Phe Leu Ser Phe Gln				
	130	135	140	
Glu Thr Thr Ile Ala Glu Ala Met Gln Ala Met Gln Ala Gln Ala Thr				
	145	150	155	160
Val Leu Glu Ile Asp Ala Ser Lys Lys Phe Ala Lys Met Gln Glu Thr				
	165	170	175	
Leu Asp Phe Ile Ala Glu Arg Leu Lys Asn Val Lys Lys Lys Lys Gly				
	180	185	190	
Val Glu Leu Phe His Lys Ala Asn Lys Ile Ser Gly His Gln Ala Ile				
	195	200	205	
Ser Ser Asp Ile Leu Glu Lys Gly Gly Ile Asp Asn Phe Gly Leu Lys				
	210	215	220	
Tyr Val Lys Phe Gly Arg Ala Asp Ile Ser Val Glu Lys Ile Val Lys				
	225	230	235	240
Glu Asn Pro Glu Ile Ile Phe Ile Trp Trp Ile Ser Pro Leu Thr Pro				
	245	250	255	
Glu Asp Val Leu Asn Asn Pro Lys Phe Ala Thr Ile Lys Ala Ile Lys				



aag ggt tat gct gat gtg ttg ggg agc gcg aaa cgg ccc gct aaa ttc 600  
 Lys Gly Tyr Ala Asp Val Leu Gly Ser Ala Lys Arg Pro Ala Lys Phe  
 145 150 155 160

gtg ttt gat atg gaa gat att aat gaa gaa aat cgt aag gct aaa ttg 648  
 Val Phe Asp Met Glu Asp Ile Asn Glu Glu Asn Arg Lys Ala Lys Leu  
 165 170 175

aag aag aaa ggc gaa aaa cca tgattgtcat taaagacgct cattttctca 699  
 Lys Lys Lys Gly Glu Lys Pro  
 180

cttctttcaag ccaacttttt caatgccctg cgagtttgac ttctgaaatg gtggtttttag 759  
 ggcgcagcaa tgtaggcaaa agctcgttta ttaatacctt g 800

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 <213> Helicobacter pylori

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 Leu Leu Glu Ile Thr Gly Asn Gln Phe Val Ala Asn Asp Lys Thr Lys  
 35 40 45  
 Thr Ala Val Ile Gln Gly Asn Val Gln Ile Lys Lys Gly Lys Asp Arg  
 50 55 60  
 Leu Phe Ala Asp Lys Val Ser Val Phe Leu Asn Asp Lys Arg Lys Pro  
 65 70 75 80  
 Glu Arg Tyr Glu Ala Thr Gly Asn Thr His Phe Asn Ile Phe Thr Glu  
 85 90 95  
 Asp Asn Arg Glu Ile Ser Gly Ser Ala Asp Lys Leu Ile Tyr Asn Ala  
 100 105 110  
 Leu Asn Gly Glu Tyr Lys Leu Leu Gln Asn Ala Val Val Arg Glu Val  
 115 120 125  
 Gly Lys Ser Asn Val Ile Thr Gly Asp Glu Ile Ile Leu Asn Lys Thr  
 130 135 140  
 Lys Gly Tyr Ala Asp Val Leu Gly Ser Ala Lys Arg Pro Ala Lys Phe  
 145 150 155 160  
 Val Phe Asp Met Glu Asp Ile Asn Glu Glu Asn Arg Lys Ala Lys Leu  
 165 170 175  
 Lys Lys Lys Gly Glu Lys Pro  
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 <212> DNA  
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 aaaaaaaggc taatactatc ataagga atg aag ttg ata aaa ttt gtg cgt aat 114

Met Lys Leu Ile Lys Phe Val Arg Asn  
1 5

gtg gtt ttg ttc att tta acg gcg atc ttt tta gcg ttc atg ctt ttg 162  
Val Val Leu Phe Ile Leu Thr Ala Ile Phe Leu Ala Phe Met Leu Leu  
10 15 20 25

gtg agt tat tgc atg ccc cat tat agc gcg gct gtc att agc ggg gtg 210  
Val Ser Tyr Cys Met Pro His Tyr Ser Ala Ala Val Ile Ser Gly Val  
30 35 40

gaa gtc aaa aga atg aat gaa aat gaa aac acg ccc aat aat aag gaa 258  
Glu Val Lys Arg Met Asn Glu Asn Glu Asn Thr Pro Asn Asn Lys Glu  
45 50 55

gta aaa acc ctt gct aga gat gtc tat ttt gtg caa act tac gac cct 306  
Val Lys Thr Leu Ala Arg Asp Val Tyr Phe Val Gln Thr Tyr Asp Pro  
60 65 70

aaa gat caa aaa agc gta acc gtt tat cgt aac gaa gac acg cgc ttt 354  
Lys Asp Gln Lys Ser Val Thr Val Tyr Arg Asn Glu Asp Thr Arg Phe  
75 80 85

agc ttc cct ttt tat ttt aag ttt aat tgc gct gat att tca gcc ctc 402  
Ser Phe Pro Phe Tyr Phe Lys Phe Asn Ser Ala Asp Ile Ser Ala Leu  
90 95 100 105

gct caa agt tta atc aat cag caa gtg gaa gtg aaa tac tat ggt tgg 450  
Ala Gln Ser Leu Ile Asn Gln Gln Val Glu Val Lys Tyr Tyr Gly Trp  
110 115 120

cgg atc aat ttg ttt aac atg ttc cct aat gtg att ttt tta aag ccc 498  
Arg Ile Asn Leu Phe Asn Met Phe Pro Asn Val Ile Phe Leu Lys Pro  
125 130 135

tta aaa gag agc act gac att tca aag ccc att ttt agc tgg att tta 546  
Leu Lys Glu Ser Thr Asp Ile Ser Lys Pro Ile Phe Ser Trp Ile Leu  
140 145 150

tac gct ttg ctg tta atg ggc ttt ttt atc agc gcg cgt tct gtt tgc 594  
Tyr Ala Leu Leu Leu Met Gly Phe Phe Ile Ser Ala Arg Ser Val Cys  
155 160 165

act tta ttt aag agc aaa gct cat taaaactttt aggctttgtt ggaaaatcac 648  
Thr Leu Phe Lys Ser Lys Ala His  
170 175

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agcgggtgttg tttcct 724

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<213> Helicobacter pylori

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Ala Ile Phe Leu Ala Phe Met Leu Leu Val Ser Tyr Cys Met Pro His





gat ttt tta aat cag gac aag cat tac gcc att atc caa aga gcg gat	464
Asp Phe Leu Asn Gln Asp Lys His Tyr Ala Ile Ile Gln Arg Ala Asp	
90 95 100	
aaa agc att tcc agt aat gaa gcg ttg gct cgt tcg ctc att ggg gcg	512
Lys Ser Ile Ser Ser Asn Glu Ala Leu Ala Arg Ser Leu Ile Gly Ala	
105 110 115	
tat gtg tta aac cga gag agt att aac cgc att gac gat aaa tcg cgc	560
Tyr Val Leu Asn Arg Glu Ser Ile Asn Arg Ile Asp Asp Lys Ser Arg	
120 125 130	
tat gaa ttg gtg cgc ttg caa agc agt tct aaa gtg tgg caa cgc ttt	608
Tyr Glu Leu Val Arg Leu Gln Ser Ser Ser Lys Val Trp Gln Arg Phe	
135 140 145	
gaa gat ttg att aaa acc caa aac agc att tat gtg caa agc cat ttg	656
Glu Asp Leu Ile Lys Thr Gln Asn Ser Ile Tyr Val Gln Ser His Leu	
150 155 160 165	
gaa aga gaa gtc cat atc gtc aat att gcg atc tat cag caa gac aat	704
Glu Arg Glu Val His Ile Val Asn Ile Ala Ile Tyr Gln Gln Asp Asn	
170 175 180	
aac ccc att gcg agc gtc tcc att gcg gct aaa ctt ttg aac gaa aac	752
Asn Pro Ile Ala Ser Val Ser Ile Ala Ala Lys Leu Leu Asn Glu Asn	
185 190 195	
aag ttg gtg tat gaa aag cgt tat aaa atc gta ttg agt tat ttg ttt	800
Lys Leu Val Tyr Glu Lys Arg Tyr Lys Ile Val Leu Ser Tyr Leu Phe	
200 205 210	
gac acc ccg gat ttt gat tac gct tcc atg cct aaa aac cct acc gga	848
Asp Thr Pro Asp Phe Asp Tyr Ala Ser Met Pro Lys Asn Pro Thr Gly	
215 220 225	
ttt aaa atc acc cgt tac agc atc act gaa atc act aat agg ggt gat	896
Phe Lys Ile Thr Arg Tyr Ser Ile Thr Glu Ile Thr Asn Arg Gly Asp	
230 235 240 245	
tgatgcgtaa ggtttttatcac gctcttgtgg gctttttgtt ggcttttagc gctttaaaag	956
ccgatgatttt tttagaagaa gcgaacgaaa cagccccggc gcatttaaac caccctatgc	1016
aggattttaa cgccattcaa gggag	1041

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 <212> PRT  
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 Ser Val Asn Asp Leu Asp Met Gln Ser Val Phe Arg Leu Glu Arg Asn  
 35 40 45  
 Arg Leu Lys Ile Ala Tyr Lys Leu Leu Gly Leu Met Ser Phe Ile Ala  
 50 55 60  
 Leu Val Leu Ala Ile Val Leu Ile Ser Val Leu Pro Leu Gln Lys Thr

65		70		75		80									
Glu	His	His	Phe	Val	Asp	Phe	Leu	Asn	Gln	Asp	Lys	His	Tyr	Ala	Ile
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Ile	Gln	Arg	Ala	Asp	Lys	Ser	Ile	Ser	Ser	Asn	Glu	Ala	Leu	Ala	Arg
		100						105					110		
Ser	Leu	Ile	Gly	Ala	Tyr	Val	Leu	Asn	Arg	Glu	Ser	Ile	Asn	Arg	Ile
		115					120					125			
Asp	Asp	Lys	Ser	Arg	Tyr	Glu	Leu	Val	Arg	Leu	Gln	Ser	Ser	Ser	Lys
	130					135					140				
Val	Trp	Gln	Arg	Phe	Glu	Asp	Leu	Ile	Lys	Thr	Gln	Asn	Ser	Ile	Tyr
145					150					155					160
Val	Gln	Ser	His	Leu	Glu	Arg	Glu	Val	His	Ile	Val	Asn	Ile	Ala	Ile
			165						170					175	
Tyr	Gln	Gln	Asp	Asn	Asn	Pro	Ile	Ala	Ser	Val	Ser	Ile	Ala	Ala	Lys
		180						185					190		
Leu	Leu	Asn	Glu	Asn	Lys	Leu	Val	Tyr	Glu	Lys	Arg	Tyr	Lys	Ile	Val
		195				200					205				
Leu	Ser	Tyr	Leu	Phe	Asp	Thr	Pro	Asp	Phe	Asp	Tyr	Ala	Ser	Met	Pro
	210				215					220					
Lys	Asn	Pro	Thr	Gly	Phe	Lys	Ile	Thr	Arg	Tyr	Ser	Ile	Thr	Glu	Ile
225				230					235					240	
Thr	Asn	Arg	Gly	Asp											
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<220>  
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 agtcattttg atttctaaaa atagtctata atgctcgcaa gagatatttt ttaagggtat 180  
 ca atg aaa gct ata aaa ata ctt ttt ata atg aca ctc agt tta aac 227  
 Met Lys Ala Ile Lys Ile Leu Phe Ile Met Thr Leu Ser Leu Asn  
 1 5 10 15  
 gct atc agc gtg aat agg gcg ttg ttt gat tta aaa gat tcg caa tta 275  
 Ala Ile Ser Val Asn Arg Ala Leu Phe Asp Leu Lys Asp Ser Gln Leu  
 20 25 30  
 aaa ggg gaa tta acg cca aaa ata gtg aat ttt ggg ggt tat aaa agc 323  
 Lys Gly Glu Leu Thr Pro Lys Ile Val Asn Phe Gly Gly Tyr Lys Ser  
 35 40 45  
 agc act gaa gag tgg ggg gct acg gct tta aac tat atc aat gcg gct 371  
 Ser Thr Glu Glu Trp Gly Ala Thr Ala Leu Asn Tyr Ile Asn Ala Ala  
 50 55 60  
 aat ggc gat gcg aaa aaa ttc agc act cta gtg gaa aaa atg cgt ttt 419  
 Asn Gly Asp Ala Lys Lys Phe Ser Thr Leu Val Glu Lys Met Arg Phe  
 65 70 75  
 aac tcc ggt ata ttg ggg aat tta aga gtg cat gca cgt ttg agg caa 467

Asn	Ser	Gly	Ile	Leu	Gly	Asn	Leu	Arg	Val	His	Ala	Arg	Leu	Arg	Gln		
80					85					90					95		
gcc	cta	aaa	ttg	caa	aag	aat	ttg	aaa	tat	tgc	ctt	aaa	atc	atc	gct	515	
Ala	Leu	Lys	Leu	Gln	Lys	Asn	Leu	Lys	Tyr	Cys	Leu	Lys	Ile	Ile	Ala		
			100						105					110			
agg	gat	tct	ttt	tat	agc	tac	cgc	acc	ggt	att	tat	atc	ccc	tta	ggc	563	
Arg	Asp	Ser	Phe	Tyr	Ser	Tyr	Arg	Thr	Gly	Ile	Tyr	Ile	Pro	Leu	Gly		
			115					120					125				
att	tct	tta	aaa	gat	caa	aaa	acg	gct	caa	aaa	atg	ctc	gct	gat	ttg	611	
Ile	Ser	Leu	Lys	Asp	Gln	Lys	Thr	Ala	Gln	Lys	Met	Leu	Ala	Asp	Leu		
		130					135					140					
agc	gtg	gta	ggg	gcg	tat	ctt	aaa	aaa	caa	caa	gag	aat	gaa	aag	gct	659	
Ser	Val	Val	Gly	Ala	Tyr	Leu	Lys	Lys	Gln	Gln	Glu	Asn	Glu	Lys	Ala		
	145					150					155						
caa	agc	cct	tat	tac	aga	aac	aac	aac	tat	tac	aac	tct	tac	tat	agc	707	
Gln	Ser	Pro	Tyr	Tyr	Arg	Asn	Asn	Asn	Tyr	Tyr	Asn	Ser	Tyr	Tyr	Ser		
160					165				170						175		
cct	tat	tac	gga	atg	tat	ggt	atg	tat	ggc	atg	ggc	atg	tat	gga	atg	755	
Pro	Tyr	Tyr	Gly	Met	Tyr	Gly	Met	Tyr	Gly	Met	Gly	Met	Tyr	Gly	Met		
			180						185					190			
tat	ggc	atg	ggc	atg	tat	gat	ttt	tat	gac	ttt	tat	gat	ggc	atg	tat	803	
Tyr	Gly	Met	Gly	Met	Tyr	Asp	Phe	Tyr	Asp	Phe	Tyr	Asp	Gly	Met	Tyr		
			195					200					205				
gga	ttc	tac	cct	aac	atg	ttt	ttc	atg	atg	caa	gtt	caa	gat	tac	ttg	851	
Gly	Phe	Tyr	Pro	Asn	Met	Phe	Phe	Met	Met	Gln	Val	Gln	Asp	Tyr	Leu		
		210					215					220					
atg	tta	gaa	aat	tac	atg	tat	gcg	ctc	gat	caa	gaa	gag	att	tta	gat	899	
Met	Leu	Glu	Asn	Tyr	Met	Tyr	Ala	Leu	Asp	Gln	Glu	Glu	Ile	Leu	Asp		
	225					230				235							
cat	gac	gct	tct	act	gac	caa	ctt	gat	acg	cct	act	gat	gat	gac	aaa	947	
His	Asp	Ala	Ser	Thr	Asp	Gln	Leu	Asp	Thr	Pro	Thr	Asp	Asp	Asp	Lys		
240					245					250					255		
gac	gat	aaa	gac	gat	aaa	tcc	tta	cag	cag	gca	aat	ctt	atg	aac	ttt	995	
Asp	Asp	Lys	Asp	Asp	Lys	Ser	Leu	Gln	Gln	Ala	Asn	Leu	Met	Asn	Phe		
			260					265						270			
tat	cgt	gat	ccc	aaa	ttc	agc	aaa	ggc	att	caa	acc	aac	cgc	ttg	aat	1043	
Tyr	Arg	Asp	Pro	Lys	Phe	Ser	Lys	Gly	Ile	Gln	Thr	Asn	Arg	Leu	Asn		
			275					280					285				
agc	gct	tta	gtc	aat	tta	gac	aac	agt	cgc	atg	ctc	aaa	gac	aat	tcg	1091	
Ser	Ala	Leu	Val	Asn	Leu	Asp	Asn	Ser	Arg	Met	Leu	Lys	Asp	Asn	Ser		
		290					295					300					
ctt	ttc	cac	act	aaa	gcc	atg	ccc	act	aaa	agc	gtg	gat	gcg	ata	act	1139	
Leu	Phe	His	Thr	Lys	Ala	Met	Pro	Thr	Lys	Ser	Val	Asp	Ala	Ile	Thr		
	305					310					315						

tct	caa	gcc	aaa	gag	ctt	aac	cat	tta	gtg	ggg	caa	atc	aaa	gaa	atg	1187
Ser	Gln	Ala	Lys	Glu	Leu	Asn	His	Leu	Val	Gly	Gln	Ile	Lys	Glu	Met	
320					325					330					335	
aag	caa	gac	ggg	gcg	agt	cct	agt	aag	att	gat	tca	gtt	gtc	aat	aaa	1235
Lys	Gln	Asp	Gly	Ala	Ser	Pro	Ser	Lys	Ile	Asp	Ser	Val	Val	Asn	Lys	
				340					345					350		
gct	atg	gaa	gtg	agg	gac	aag	cta	gac	aat	aat	ctc	aac	caa	cta	gac	1283
Ala	Met	Glu	Val	Arg	Asp	Lys	Leu	Asp	Asn	Asn	Leu	Asn	Gln	Leu	Asp	
			355					360					365			
aat	gac	tta	aaa	gat	caa	aaa	ggg	ctt	tca	agc	gag	caa	caa	gct	caa	1331
Asn	Asp	Leu	Lys	Asp	Gln	Lys	Gly	Leu	Ser	Ser	Glu	Gln	Gln	Ala	Gln	
		370					375					380				
gtg	gat	aaa	gcc	cta	gac	agc	gtg	caa	caa	tta	agc	cat	agc	agc	gat	1379
Val	Asp	Lys	Ala	Leu	Asp	Ser	Val	Gln	Gln	Leu	Ser	His	Ser	Ser	Asp	
	385					390					395					
gtg	gtg	ggg	aat	tat	tta	gac	ggg	agt	ttg	aaa	att	gat	ggc	gat	gat	1427
Val	Val	Gly	Asn	Tyr	Leu	Asp	Gly	Ser	Leu	Lys	Ile	Asp	Gly	Asp	Asp	
400					405					410				415		
aga	gat	gat	ttg	aat	gat	gcg	atg	aat	aac	cct	atg	caa	caa	ccc	gtg	1475
Arg	Asp	Asp	Leu	Asn	Asp	Ala	Met	Asn	Asn	Pro	Met	Gln	Gln	Pro	Val	
				420					425					430		
caa	caa	acg	cct	act	agc	aac	atg	gcc	gac	acc	cat	gca	aat	gac	agc	1523
Gln	Gln	Thr	Pro	Thr	Ser	Asn	Met	Ala	Asp	Thr	His	Ala	Asn	Asp	Ser	
			435					440					445			
aag	gat	caa	ggg	agt	aac	gcg	ctc	ata	aac	cct	aac	agc	gcc	act	aac	1571
Lys	Asp	Gln	Gly	Ser	Asn	Ala	Leu	Ile	Asn	Pro	Asn	Ser	Ala	Thr	Asn	
		450					455					460				
gcc	gac	gac	act	cac	act	gac	gat	act	cac	act	gac	act	aac	acc	aca	1619
Ala	Asp	Asp	Thr	His	Thr	Asp	Asp	Thr	His	Thr	Asp	Thr	Asn	Thr	Thr	
	465					470					475					
aac	gat	gct	agc	acc	act	gac	acc	ccc	act	gac	gat	aaa	gat	gct	agc	1667
Asn	Asp	Ala	Ser	Thr	Thr	Asp	Thr	Pro	Thr	Asp	Asp	Lys	Asp	Ala	Ser	
480					485					490					495	
ggc	ttg	aac	aat	acc	ggc	gat	atg	aat	aac	acg	gat	acc	ggc	aac	acg	1715
Gly	Leu	Asn	Asn	Thr	Gly	Asp	Met	Asn	Asn	Thr	Asp	Thr	Gly	Asn	Thr	
				500					505					510		
gac	acc	ggc	aat	acg	gat	acc	ggt	aac	act	gat	gat	atg	agc	aac	atg	1763
Asp	Thr	Gly	Asn	Thr	Asp	Thr	Gly	Asn	Thr	Asp	Asp	Met	Ser	Asn	Met	
			515					520					525			
aac	aac	ggc	aac	gat	gat	acg	ggt	aac	gct	aat	gac	gac	atg	agc	aac	1811
Asn	Asn	Gly	Asn	Asp	Asp	Thr	Gly	Asn	Ala	Asn	Asp	Asp	Met	Ser	Asn	
		530					535					540				
ggc	aac	gac	atg	ggc	gat	gat	ttg	aac	aac	gcg	aac	gat	atg	aac	gac	1859
Gly	Asn	Asp	Met	Gly	Asp	Asp	Leu	Asn	Asn	Ala	Asn	Asp	Met	Asn	Asp	
	545				550						555					

gac atg ggt aat ggc aac gat gac atg ggc gat atg ggg gat atg aac 1907  
 Asp Met Gly Asn Gly Asn Asp Asp Met Gly Asp Met Gly Asp Met Asn  
 560 565 570 575

gac gat atg ggt ggc gat atg gga gac atg ggg gat atg ggc gat atg 1955  
 Asp Asp Met Gly Gly Asp Met Gly Asp Met Gly Asp Met Gly Asp Met  
 580 585 590

ggg aat tgagattaac cccaatatca aagagtata gccaaaactt taaggaatat 2011  
 Gly Asn

ttttatagta aaaacgattc ttttaaggta atagggggga tattttgc 2059

<210> 66  
 <211> 593  
 <212> PRT  
 <213> Helicobacter pylori

<400> 66  
 Met Lys Ala Ile Lys Ile Leu Phe Ile Met Thr Leu Ser Leu Asn Ala  
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 Ile Ser Val Asn Arg Ala Leu Phe Asp Leu Lys Asp Ser Gln Leu Lys  
 20 25 30  
 Gly Glu Leu Thr Pro Lys Ile Val Asn Phe Gly Gly Tyr Lys Ser Ser  
 35 40 45  
 Thr Glu Glu Trp Gly Ala Thr Ala Leu Asn Tyr Ile Asn Ala Ala Asn  
 50 55 60  
 Gly Asp Ala Lys Lys Phe Ser Thr Leu Val Glu Lys Met Arg Phe Asn  
 65 70 75 80  
 Ser Gly Ile Leu Gly Asn Leu Arg Val His Ala Arg Leu Arg Gln Ala  
 85 90 95  
 Leu Lys Leu Gln Lys Asn Leu Lys Tyr Cys Leu Lys Ile Ile Ala Arg  
 100 105 110  
 Asp Ser Phe Tyr Ser Tyr Arg Thr Gly Ile Tyr Ile Pro Leu Gly Ile  
 115 120 125  
 Ser Leu Lys Asp Gln Lys Thr Ala Gln Lys Met Leu Ala Asp Leu Ser  
 130 135 140  
 Val Val Gly Ala Tyr Leu Lys Lys Gln Gln Glu Lys Ala Gln  
 145 150 155 160  
 Ser Pro Tyr Tyr Arg Asn Asn Asn Tyr Tyr Asn Ser Tyr Tyr Ser Pro  
 165 170 175  
 Tyr Tyr Gly Met Tyr Gly Met Tyr Gly Met Gly Met Tyr Gly Met Tyr  
 180 185 190  
 Gly Met Gly Met Tyr Asp Phe Tyr Asp Phe Tyr Asp Gly Met Tyr Gly  
 195 200 205  
 Phe Tyr Pro Asn Met Phe Phe Met Met Gln Val Gln Asp Tyr Leu Met  
 210 215 220  
 Leu Glu Asn Tyr Met Tyr Ala Leu Asp Gln Glu Glu Ile Leu Asp His  
 225 230 235 240  
 Asp Ala Ser Thr Asp Gln Leu Asp Thr Pro Thr Asp Asp Asp Lys Asp  
 245 250 255  
 Asp Lys Asp Asp Lys Ser Leu Gln Gln Ala Asn Leu Met Asn Phe Tyr  
 260 265 270  
 Arg Asp Pro Lys Phe Ser Lys Gly Ile Gln Thr Asn Arg Leu Asn Ser  
 275 280 285  
 Ala Leu Val Asn Leu Asp Asn Ser Arg Met Leu Lys Asp Asn Ser Leu  
 290 295 300

Phe His Thr Lys Ala Met Pro Thr Lys Ser Val Asp Ala Ile Thr Ser  
 305 310 315 320  
 Gln Ala Lys Glu Leu Asn His Leu Val Gly Gln Ile Lys Glu Met Lys  
 325 330 335  
 Gln Asp Gly Ala Ser Pro Ser Lys Ile Asp Ser Val Val Asn Lys Ala  
 340 345 350  
 Met Glu Val Arg Asp Lys Leu Asp Asn Asn Leu Asn Gln Leu Asp Asn  
 355 360 365  
 Asp Leu Lys Asp Gln Lys Gly Leu Ser Ser Glu Gln Gln Ala Gln Val  
 370 375 380  
 Asp Lys Ala Leu Asp Ser Val Gln Gln Leu Ser His Ser Ser Asp Val  
 385 390 395 400  
 Val Gly Asn Tyr Leu Asp Gly Ser Leu Lys Ile Asp Gly Asp Asp Arg  
 405 410 415  
 Asp Asp Leu Asn Asp Ala Met Asn Asn Pro Met Gln Gln Pro Val Gln  
 420 425 430  
 Gln Thr Pro Thr Ser Asn Met Ala Asp Thr His Ala Asn Asp Ser Lys  
 435 440 445  
 Asp Gln Gly Ser Asn Ala Leu Ile Asn Pro Asn Ser Ala Thr Asn Ala  
 450 455 460  
 Asp Asp Thr His Thr Asp Asp Thr His Thr Asp Thr Asn Thr Thr Asn  
 465 470 475 480  
 Asp Ala Ser Thr Thr Asp Thr Pro Thr Asp Asp Lys Asp Ala Ser Gly  
 485 490 495  
 Leu Asn Asn Thr Gly Asp Met Asn Asn Thr Asp Thr Gly Asn Thr Asp  
 500 505 510  
 Thr Gly Asn Thr Asp Thr Gly Asn Thr Asp Asp Met Ser Asn Met Asn  
 515 520 525  
 Asn Gly Asn Asp Asp Thr Gly Asn Ala Asn Asp Asp Met Ser Asn Gly  
 530 535 540  
 Asn Asp Met Gly Asp Asp Leu Asn Asn Ala Asn Asp Met Asn Asp Asp  
 545 550 555 560  
 Met Gly Asn Gly Asn Asp Asp Met Gly Asp Met Gly Asp Met Asn Asp  
 565 570 575  
 Asp Met Gly Gly Asp Met Gly Asp Met Gly Asp Met Gly Asp Met Gly  
 580 585 590  
 Asn

<210> 67  
 <211> 1527  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (112)...(1461)

<400> 67  
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 Met Ser  
 1

atg gaa ttt gat gct gtt att att gga ggt ggg gtt tca ggg tgc gcg 165  
 Met Glu Phe Asp Ala Val Ile Ile Gly Gly Gly Val Ser Gly Cys Ala  
 5 10 15

acc ttt tat act ttg agc gaa tac agc tct tta aag cgc gtg gct atc	213
Thr Phe Tyr Thr Leu Ser Glu Tyr Ser Ser Leu Lys Arg Val Ala Ile	
20 25 30	
gtg gaa aaa tgc tct aaa ttg gct caa atc agc tcc agc gct aaa gct	261
Val Glu Lys Cys Ser Lys Leu Ala Gln Ile Ser Ser Ser Ala Lys Ala	
35 40 45 50	
aat tcg caa acc att cat gat ggc tct att gaa acg aat tac act ccc	309
Asn Ser Gln Thr Ile His Asp Gly Ser Ile Glu Thr Asn Tyr Thr Pro	
55 60 65	
gaa aaa gct aaa aaa gtg cgt ttg agc gct tat aag acc agg caa tac	357
Glu Lys Ala Lys Lys Val Arg Leu Ser Ala Tyr Lys Thr Arg Gln Tyr	
70 75 80	
gct ttg aat aaa ggc ttg caa aat gaa gtg att ttt gaa acc cag aaa	405
Ala Leu Asn Lys Gly Leu Gln Asn Glu Val Ile Phe Glu Thr Gln Lys	
85 90 95	
atg gct ata ggc gtg ggc gat gaa gaa tgc gag ttc atg aaa aaa cgc	453
Met Ala Ile Gly Val Gly Asp Glu Glu Cys Glu Phe Met Lys Lys Arg	
100 105 110	
tac gaa tct ttt aaa gaa atc ttt gtg ggg tta gaa gaa ttt gac aag	501
Tyr Glu Ser Phe Lys Glu Ile Phe Val Gly Leu Glu Glu Phe Asp Lys	
115 120 125 130	
caa aag att aaa gaa tta gag cct aat gtg att tta ggg gct aat ggc	549
Gln Lys Ile Lys Glu Leu Glu Pro Asn Val Ile Leu Gly Ala Asn Gly	
135 140 145	
ata gac agg cat gaa aac att atc ggg cat ggg tat aga aag gat tgg	597
Ile Asp Arg His Glu Asn Ile Ile Gly His Gly Tyr Arg Lys Asp Trp	
150 155 160	
agc acc atg aat ttt gcg aag ttg agt gaa aac ttc gtt gaa gaa gcc	645
Ser Thr Met Asn Phe Ala Lys Leu Ser Glu Asn Phe Val Glu Glu Ala	
165 170 175	
cta aaa tta aag cct aac aac cag gtg ttt ttg aat ttc aaa gtg aaa	693
Leu Lys Leu Lys Pro Asn Asn Gln Val Phe Leu Asn Phe Lys Val Lys	
180 185 190	
aag att gaa aaa cgc aac gac act tac gcc gta att tca gaa gac gct	741
Lys Ile Glu Lys Arg Asn Asp Thr Tyr Ala Val Ile Ser Glu Asp Ala	
195 200 205 210	
gaa gaa gtg tat gct aaa ttc gtg ctg gtc aat gcc ggc tct tac gct	789
Glu Glu Val Tyr Ala Lys Phe Val Leu Val Asn Ala Gly Ser Tyr Ala	
215 220 225	
ttg cct ttg gct cag agc atg ggc tat ggc cta gat tta ggg tgc ttg	837
Leu Pro Leu Ala Gln Ser Met Gly Tyr Gly Leu Asp Leu Gly Cys Leu	
230 235 240	
cct gtg gcg ggc agc ttt tat ttt gtg ccg gat tta tta agg ggt aag	885
Pro Val Ala Gly Ser Phe Tyr Phe Val Pro Asp Leu Leu Arg Gly Lys	
245 250 255	

gtt tat acc gtt caa aac ccc aaa ctc cct ttt gca gcc gtg cat ggc	933
Val Tyr Thr Val Gln Asn Pro Lys Leu Pro Phe Ala Ala Val His Gly	
260 265 270	
gac cct gat gcc gtc att aaa gga aaa aca cga atc ggg cct acc gct	981
Asp Pro Asp Ala Val Ile Lys Gly Lys Thr Arg Ile Gly Pro Thr Ala	
275 280 285 290	
tta acg atg cct aaa tta gaa cgc aac aaa tgt tgg ctt aag ggc att	1029
Leu Thr Met Pro Lys Leu Glu Arg Asn Lys Cys Trp Leu Lys Gly Ile	
295 300 305	
agc ttg gaa ttg ttg aaa atg gat ttg aat aaa gat gtg ttt aaa att	1077
Ser Leu Glu Leu Lys Met Asp Leu Asn Lys Asp Val Phe Lys Ile	
310 315 320	
gcg ttt gat ttg atg agc gat aaa gaa atc cga aat tat gtg ttt aaa	1125
Ala Phe Asp Leu Met Ser Asp Lys Glu Ile Arg Asn Tyr Val Phe Lys	
325 330 335	
aac atg gtt ttt gaa ttg ccc att atc ggt aaa agg aaa ttt tta aaa	1173
Asn Met Val Phe Glu Leu Pro Ile Ile Gly Lys Arg Lys Phe Leu Lys	
340 345 350	
gac gct caa aaa atc atc ccc tct ctt agc cta gaa gat cta gaa tac	1221
Asp Ala Gln Lys Ile Ile Pro Ser Leu Ser Leu Glu Asp Leu Glu Tyr	
355 360 365 370	
gct cat ggt ttt ggt gaa gtg cgc ccg caa gtt tta gac aga acc aag	1269
Ala His Gly Phe Gly Glu Val Arg Pro Gln Val Leu Asp Arg Thr Lys	
375 380 385	
cga aaa ctg gaa tta ggc gaa aaa aag att tgc acc cat aaa ggc atc	1317
Arg Lys Leu Glu Leu Gly Glu Lys Lys Ile Cys Thr His Lys Gly Ile	
390 395 400	
act ttt aac atg acc cct tct cca ggc gcg acg agt tgt ttg caa aac	1365
Thr Phe Asn Met Thr Pro Ser Pro Gly Ala Thr Ser Cys Leu Gln Asn	
405 410 415	
gcc ctt gtg gat tcc caa gaa atc gct gcg tat ttg ggc gag agc ttt	1413
Ala Leu Val Asp Ser Gln Glu Ile Ala Ala Tyr Leu Gly Glu Ser Phe	
420 425 430	
gaa tta gaa cgc ttt tat aaa gat tta tcc cca gaa gaa ttg gaa aat	1461
Glu Leu Glu Arg Phe Tyr Lys Asp Leu Ser Pro Glu Glu Leu Glu Asn	
435 440 445 450	
taaaaacgca tgcaaaaaga acaagaagcc caagaaatcg ctaaaaaagc cgttaaaatc	1521
gtgttt	1527

<210> 68  
 <211> 450  
 <212> PRT  
 <213> Helicobacter pylori

<400> 68  
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Cys	Ala	Thr	Phe	Tyr	Thr	Leu	Ser
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Ala	Ile	Val	Glu	Lys	Cys	Ser	Lys
		35				40	
Lys	Ala	Asn	Ser	Gln	Thr	Ile	His
		50				55	
Thr	Pro	Glu	Lys	Ala	Lys	Lys	Val
		65				70	
Gln	Tyr	Ala	Leu	Asn	Lys	Gly	Leu
				85			90
Gln	Lys	Met	Ala	Ile	Gly	Val	Gly
		100					105
Lys	Arg	Tyr	Glu	Ser	Phe	Lys	Glu
		115					120
Asp	Lys	Gln	Lys	Ile	Lys	Glu	Leu
		130				135	
Asn	Gly	Ile	Asp	Arg	His	Glu	Asn
		145				150	
Asp	Trp	Ser	Thr	Met	Asn	Phe	Ala
				165			170
Glu	Ala	Leu	Lys	Leu	Lys	Pro	Asn
		180					185
Val	Lys	Lys	Ile	Glu	Lys	Arg	Asn
		195					200
Asp	Ala	Glu	Glu	Val	Tyr	Ala	Lys
		210				215	
Tyr	Ala	Leu	Pro	Leu	Ala	Gln	Ser
		225				230	
Cys	Leu	Pro	Val	Ala	Gly	Ser	Phe
				245			250
Gly	Lys	Val	Tyr	Thr	Val	Gln	Asn
		260					265
His	Gly	Asp	Pro	Asp	Ala	Val	Ile
		275				280	
Thr	Ala	Leu	Thr	Met	Pro	Lys	Leu
		290				295	
Gly	Ile	Ser	Leu	Glu	Leu	Lys	Met
		305				310	
Lys	Ile	Ala	Phe	Asp	Leu	Met	Ser
				325			330
Phe	Lys	Asn	Met	Val	Phe	Glu	Leu
		340				345	
Leu	Lys	Asp	Ala	Gln	Lys	Ile	Ile
		355				360	
Glu	Tyr	Ala	His	Gly	Phe	Gly	Glu
		370				375	
Thr	Lys	Arg	Lys	Leu	Glu	Leu	Gly
		385				390	
Gly	Ile	Thr	Phe	Asn	Met	Thr	Pro
				405			410
Gln	Asn	Ala	Leu	Val	Asp	Ser	Gln
		420					425
Ser	Phe	Glu	Leu	Glu	Arg	Phe	Tyr
		435				440	
Glu	Asn						
		450					

<210> 69  
 <211> 653  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (63)...(590)

<400> 69  
 ctagatttttaa ttttaaagtt atataattaa accacaaaat ctttttttaa aagaaactaa 60  
 gc atg cca aaa ccc aag aaa aac acc ctc ccc tgt agc ctt tct gtc 107  
 Met Pro Lys Pro Lys Lys Asn Thr Leu Pro Cys Ser Leu Ser Val  
 1 5 10 15

aaa atg tct tat ttc atg cgc ttt ctc att aaa tgg cgc acc cgc tct 155  
 Lys Met Ser Tyr Phe Met Arg Phe Leu Ile Lys Trp Arg Thr Arg Ser  
 20 25 30

tta agc cat aaa atg atg act ctc att caa atc tta agc att ctg gct 203  
 Leu Ser His Lys Met Met Thr Leu Ile Gln Ile Leu Ser Ile Leu Ala  
 35 40 45

tta gcg agc aag gcc agt gaa gat tta gaa gag caa ctc aaa aaa atc 251  
 Leu Ala Ser Lys Ala Ser Glu Asp Leu Glu Glu Gln Leu Lys Lys Ile  
 50 55 60

aaa gat tac att tat aga acc cta aac gct aaa atc gca tcg gat gtg 299  
 Lys Asp Tyr Ile Tyr Arg Thr Leu Asn Ala Lys Ile Ala Ser Asp Val  
 65 70 75

tat aac cga gtg ctt att tta gtg aat gaa tat tgc act aat gaa gaa 347  
 Tyr Asn Arg Val Leu Ile Leu Val Asn Glu Tyr Cys Thr Asn Glu Glu  
 80 85 90 95

ttg ttt gac aaa gag agc gtt aaa att tca gat tta ctc att caa gac 395  
 Leu Phe Asp Lys Glu Ser Val Lys Ile Ser Asp Leu Leu Ile Gln Asp  
 100 105 110

att cag ctt tac gct tta gtg gat gaa atg ctt aaa gaa gat aaa tat 443  
 Ile Gln Leu Tyr Ala Leu Val Asp Glu Met Leu Lys Glu Asp Lys Tyr  
 115 120 125

caa gtc cag cac acc att tta aag ggc atc atc aaa cgc aaa tac gat 491  
 Gln Val Gln His Thr Ile Leu Lys Gly Ile Ile Lys Arg Lys Tyr Asp  
 130 135 140

gaa gcc tac tcg ctc aat agc gaa gac agg att ctt tta gaa tac caa 539  
 Glu Ala Tyr Ser Leu Asn Ser Glu Asp Arg Ile Leu Leu Glu Tyr Gln  
 145 150 155

gaa cgc ttg cta gaa cac tca cac gcg tct ttt tca aat aaa aaa ttc 587  
 Glu Arg Leu Leu Glu His Ser His Ala Ser Phe Ser Asn Lys Lys Phe  
 160 165 170 175

aaa tgatttgaaa gcgttacttg ccttgctttt tgggctttta ttgaaaaagg 640  
 Lys

gcttttaaaat gag

653

<210> 70  
<211> 176  
<212> PRT  
<213> Helicobacter pylori

<400> 70  
Met Pro Lys Pro Lys Lys Asn Thr Leu Pro Cys Ser Leu Ser Val Lys  
1 5 10 15  
Met Ser Tyr Phe Met Arg Phe Leu Ile Lys Trp Arg Thr Arg Ser Leu  
20 25 30  
Ser His Lys Met Met Thr Leu Ile Gln Ile Leu Ser Ile Leu Ala Leu  
35 40 45  
Ala Ser Lys Ala Ser Glu Asp Leu Glu Glu Gln Leu Lys Lys Ile Lys  
50 55 60  
Asp Tyr Ile Tyr Arg Thr Leu Asn Ala Lys Ile Ala Ser Asp Val Tyr  
65 70 75 80  
Asn Arg Val Leu Ile Leu Val Asn Glu Tyr Cys Thr Asn Glu Glu Leu  
85 90 95  
Phe Asp Lys Glu Ser Val Lys Ile Ser Asp Leu Leu Ile Gln Asp Ile  
100 105 110  
Gln Leu Tyr Ala Leu Val Asp Glu Met Leu Lys Glu Asp Lys Tyr Gln  
115 120 125  
Val Gln His Thr Ile Leu Lys Gly Ile Ile Lys Arg Lys Tyr Asp Glu  
130 135 140  
Ala Tyr Ser Leu Asn Ser Glu Asp Arg Ile Leu Leu Glu Tyr Gln Glu  
145 150 155 160  
Arg Leu Leu Glu His Ser His Ala Ser Phe Ser Asn Lys Lys Phe Lys  
165 170 175

<210> 71  
<211> 1840  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (91)...(1833)

<400> 71  
aagcggttaaa ttccaatcaa aaaccatcgt atcggtgtta atattgtgta aaaattaatg 60  
ttatgaatct cttgtattaa aaggacttca atg aaa aaa ttg gtt tta gtc atc 114  
Met Lys Lys Leu Val Leu Val Ile  
1 5  
ttt tta acg cta gcg ctt tca ata tct gca aaa gaa gtc aaa ata gtg 162  
Phe Leu Thr Leu Ala Leu Ser Ile Ser Ala Lys Glu Val Lys Ile Val  
10 15 20  
ttt tta gaa act tca gac att cat ggg cgg ctt ttt tcg tat gat tat 210  
Phe Leu Glu Thr Ser Asp Ile His Gly Arg Leu Phe Ser Tyr Asp Tyr  
25 30 35 40  
gcg att ggc gag caa aaa ccc aat aac ggc ttg aca agg att gcg act 258  
Ala Ile Gly Glu Gln Lys Pro Asn Asn Gly Leu Thr Arg Ile Ala Thr  
45 50 55

tta atc aaa aag caa agg gct gag aat aaa aat gtg gtt ttg att gac	306
Leu Ile Lys Lys Gln Arg Ala Glu Asn Lys Asn Val Val Leu Ile Asp	
60 65 70	
agc ggg gat ttg ttg caa ggc aat agc gcg gag ttg ttt aat gat gag	354
Ser Gly Asp Leu Leu Gln Gly Asn Ser Ala Glu Leu Phe Asn Asp Glu	
75 80 85	
cca att cat ccg cta gtt aga gct gaa aac gat ttg aaa ttt gac att	402
Pro Ile His Pro Leu Val Arg Ala Glu Asn Asp Leu Lys Phe Asp Ile	
90 95 100	
cgt gtg ctt ggc aat cac gag ttt aat ttc agt aaa gat ttt tta gaa	450
Arg Val Leu Gly Asn His Glu Phe Asn Phe Ser Lys Asp Phe Leu Glu	
105 110 115 120	
aag aat att aag ggg ttt aat ggc gat gtc atg aat gcg aat atc att	498
Lys Asn Ile Lys Gly Phe Asn Gly Asp Val Met Asn Ala Asn Ile Ile	
125 130 135	
aaa att gcg gac aat aag ccg ttt gta aaa cct tat att att aaa aaa	546
Lys Ile Ala Asp Asn Lys Pro Phe Val Lys Pro Tyr Ile Ile Lys Lys	
140 145 150	
att gat ggc gtg agg gtg gcg gtt gtg ggg tat gtg gtg gcg cac atc	594
Ile Asp Gly Val Arg Val Ala Val Val Gly Tyr Val Val Ala His Ile	
155 160 165	
cca act tgg gag gcc tct acg cct gaa cat ttt gca gga ttg aag ttt	642
Pro Thr Trp Glu Ala Ser Thr Pro Glu His Phe Ala Gly Leu Lys Phe	
170 175 180	
ttg gac gct gaa gaa gcg tta aaa aag acc tta aaa gag ttg aaa ggg	690
Leu Asp Ala Glu Glu Ala Leu Lys Lys Thr Leu Lys Glu Leu Lys Gly	
185 190 195 200	
aag tat gat att ttg att ggc gct ttt cat ttg ggg cga gaa gat gag	738
Lys Tyr Asp Ile Leu Ile Gly Ala Phe His Leu Gly Arg Glu Asp Glu	
205 210 215	
aaa ggt ggc gac ggg ata ccg gat tta gcg aaa aaa ttc ccg caa ttt	786
Lys Gly Gly Asp Gly Ile Pro Asp Leu Ala Lys Lys Phe Pro Gln Phe	
220 225 230	
gac atc att ttt gca ggg cat gag cat gcg gtt tat aac acc aaa gta	834
Asp Ile Ile Phe Ala Gly His Glu His Ala Val Tyr Asn Thr Lys Val	
235 240 245	
ggg aaa gtg cat acc att gag cct gga gcg tat ggg gct tat ctg gca	882
Gly Lys Val His Thr Ile Glu Pro Gly Ala Tyr Gly Ala Tyr Leu Ala	
250 255 260	
aag ggc gtg gtg gta ttt gac act aaa acg aag aaa aaa att ata acg	930
Lys Gly Val Val Val Phe Asp Thr Lys Thr Lys Lys Lys Ile Ile Thr	
265 270 275 280	
act gaa aat tta ccc aca aaa gat gtg cca gaa gat gaa gaa tta gcg	978
Thr Glu Asn Leu Pro Thr Lys Asp Val Pro Glu Asp Glu Glu Leu Ala	
285 290 295	

aaa aaa tac gaa tat gtg gat aaa aaa tca aaa gaa tac gct aat gaa	1026
Lys Lys Tyr Glu Tyr Val Asp Lys Lys Ser Lys Glu Tyr Ala Asn Glu	
300 305 310	
gtg gtt ggc gaa gtt aca aaa acc ttt att gac agg cct gat ttt atc	1074
Val Val Gly Glu Val Thr Lys Thr Phe Ile Asp Arg Pro Asp Phe Ile	
315 320 325	
aca gga gaa gaa aaa atc acc acg atg ccc acc gcc gcc ttg caa gaa	1122
Thr Gly Glu Glu Lys Ile Thr Thr Met Pro Thr Ala Ala Leu Gln Glu	
330 335 340	
aca ccg gtg ata gaa ttg att aat aaa gtg caa aaa tat tac gca aaa	1170
Thr Pro Val Ile Glu Leu Ile Asn Lys Val Gln Lys Tyr Tyr Ala Lys	
345 350 355 360	
gcc gat gtt tca gcg gca gcc tta ttc aat ttt ggg gcg aat ttg aaa	1218
Ala Asp Val Ser Ala Ala Ala Leu Phe Asn Phe Gly Ala Asn Leu Lys	
365 370 375	
aaa ggg cct ttc aaa aga aaa gat gtc act tat att tac aag ttc gct	1266
Lys Gly Pro Phe Lys Arg Lys Asp Val Thr Tyr Ile Tyr Lys Phe Ala	
380 385 390	
aat acg ctc att gga gtg cgt ata acg ggt gaa aat ctg ttg aaa tac	1314
Asn Thr Leu Ile Gly Val Arg Ile Thr Gly Glu Asn Leu Leu Lys Tyr	
395 400 405	
atg gaa tgg tca tac cga ttt tac aat cag ttg caa cca gga gat ttg	1362
Met Glu Trp Ser Tyr Arg Phe Tyr Asn Gln Leu Gln Pro Gly Asp Leu	
410 415 420	
acg atc agt ttt aat gaa aac att cgc ggc tat aac ttt gat atg ttt	1410
Thr Ile Ser Phe Asn Glu Asn Ile Arg Gly Tyr Asn Phe Asp Met Phe	
425 430 435 440	
tct ggc gtg aaa tac cag gtt gat gtt aca aaa ccc gcc gga caa agg	1458
Ser Gly Val Lys Tyr Gln Val Asp Val Thr Lys Pro Ala Gly Gln Arg	
445 450 455	
att atc aat ccg aca atc aac aac aaa ccc att gac ccc aaa gcc atc	1506
Ile Ile Asn Pro Thr Ile Asn Asn Lys Pro Ile Asp Pro Lys Ala Ile	
460 465 470	
tat aaa tta gcg atc aac aat tac cga ttc gga aca tta tcc acg aca	1554
Tyr Lys Leu Ala Ile Asn Asn Tyr Arg Phe Gly Thr Leu Ser Thr Thr	
475 480 485	
ttg aat ttg gtt aca gac gct gmt agg tat tat aat tct tac gat gaa	1602
Leu Asn Leu Val Thr Asp Ala Xaa Arg Tyr Tyr Asn Ser Tyr Asp Glu	
490 495 500	
ctg caa gat aat ggg caa ata cga gat ttg atc atc aaa tac atc acg	1650
Leu Gln Asp Asn Gly Gln Ile Arg Asp Leu Ile Ile Lys Tyr Ile Thr	
505 510 515 520	
gaa gaa aaa ggt ggg aag gta acc cct gaa ttg gag ggt aat tgg gaa	1698
Glu Glu Lys Gly Gly Lys Val Thr Pro Glu Leu Glu Gly Asn Trp Glu	

525										530					535					
atc	atc	aac	tac	gat	ttc	aaa	aac	ccg	ttg	ttg	gaa	aaa	ttg	aga	gaa	1746				
Ile	Ile	Asn	Tyr	Asp	Phe	Lys	Asn	Pro	Leu	Leu	Glu	Lys	Leu	Arg	Glu					
		540						545					550							
aaa	tta	aaa	gag	ggg	agc	atc	aaa	atc	ccc	acc	tca	aag	gat	ggg	agg	1794				
Lys	Leu	Lys	Glu	Gly	Ser	Ile	Lys	Ile	Pro	Thr	Ser	Lys	Asp	Gly	Arg					
		555					560					565								
act	ttg	aat	gtc	aaa	tcc	att	aaa	gag	agt	gaa	gtt	aaa	taaaatt			1840				
Thr	Leu	Asn	Val	Lys	Ser	Ile	Lys	Glu	Ser	Glu	Val	Lys								
	570					575					580									

<210> 72  
 <211> 581  
 <212> PRT  
 <213> Helicobacter pylori

<400> 72

Met	Lys	Lys	Leu	Val	Leu	Val	Ile	Phe	Leu	Thr	Leu	Ala	Leu	Ser	Ile
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Ser	Ala	Lys	Glu	Val	Lys	Ile	Val	Phe	Leu	Glu	Thr	Ser	Asp	Ile	His
		20						25				30			
Gly	Arg	Leu	Phe	Ser	Tyr	Asp	Tyr	Ala	Ile	Gly	Glu	Gln	Lys	Pro	Asn
	35					40					45				
Asn	Gly	Leu	Thr	Arg	Ile	Ala	Thr	Leu	Ile	Lys	Lys	Gln	Arg	Ala	Glu
	50				55					60					
Asn	Lys	Asn	Val	Val	Leu	Ile	Asp	Ser	Gly	Asp	Leu	Leu	Gln	Gly	Asn
65			70						75				80		
Ser	Ala	Glu	Leu	Phe	Asn	Asp	Glu	Pro	Ile	His	Pro	Leu	Val	Arg	Ala
			85					90					95		
Glu	Asn	Asp	Leu	Lys	Phe	Asp	Ile	Arg	Val	Leu	Gly	Asn	His	Glu	Phe
	100						105					110			
Asn	Phe	Ser	Lys	Asp	Phe	Leu	Glu	Lys	Asn	Ile	Lys	Gly	Phe	Asn	Gly
	115					120					125				
Asp	Val	Met	Asn	Ala	Asn	Ile	Ile	Lys	Ile	Ala	Asp	Asn	Lys	Pro	Phe
	130				135					140					
Val	Lys	Pro	Tyr	Ile	Ile	Lys	Lys	Ile	Asp	Gly	Val	Arg	Val	Ala	Val
145				150					155					160	
Val	Gly	Tyr	Val	Val	Ala	His	Ile	Pro	Thr	Trp	Glu	Ala	Ser	Thr	Pro
			165					170						175	
Glu	His	Phe	Ala	Gly	Leu	Lys	Phe	Leu	Asp	Ala	Glu	Glu	Ala	Leu	Lys
		180					185					190			
Lys	Thr	Leu	Lys	Glu	Leu	Lys	Gly	Lys	Tyr	Asp	Ile	Leu	Ile	Gly	Ala
	195					200					205				
Phe	His	Leu	Gly	Arg	Glu	Asp	Glu	Lys	Gly	Gly	Asp	Gly	Ile	Pro	Asp
	210				215					220					
Leu	Ala	Lys	Lys	Phe	Pro	Gln	Phe	Asp	Ile	Ile	Phe	Ala	Gly	His	Glu
225				230					235					240	
His	Ala	Val	Tyr	Asn	Thr	Lys	Val	Gly	Lys	Val	His	Thr	Ile	Glu	Pro
			245					250					255		
Gly	Ala	Tyr	Gly	Ala	Tyr	Leu	Ala	Lys	Gly	Val	Val	Val	Phe	Asp	Thr
		260				265						270			
Lys	Thr	Lys	Lys	Lys	Ile	Ile	Thr	Thr	Glu	Asn	Leu	Pro	Thr	Lys	Asp
	275					280					285				
Val	Pro	Glu	Asp	Glu	Glu	Leu	Ala	Lys	Lys	Tyr	Glu	Tyr	Val	Asp	Lys
	290				295						300				

Lys Ser Lys Glu Tyr Ala Asn Glu Val Val Gly Glu Val Thr Lys Thr  
 305 310 315 320  
 Phe Ile Asp Arg Pro Asp Phe Ile Thr Gly Glu Glu Lys Ile Thr Thr  
 325 330 335  
 Met Pro Thr Ala Ala Leu Gln Glu Thr Pro Val Ile Glu Leu Ile Asn  
 340 345 350  
 Lys Val Gln Lys Tyr Tyr Ala Lys Ala Asp Val Ser Ala Ala Ala Leu  
 355 360 365  
 Phe Asn Phe Gly Ala Asn Leu Lys Lys Gly Pro Phe Lys Arg Lys Asp  
 370 375 380  
 Val Thr Tyr Ile Tyr Lys Phe Ala Asn Thr Leu Ile Gly Val Arg Ile  
 385 390 395 400  
 Thr Gly Glu Asn Leu Leu Lys Tyr Met Glu Trp Ser Tyr Arg Phe Tyr  
 405 410 415  
 Asn Gln Leu Gln Pro Gly Asp Leu Thr Ile Ser Phe Asn Glu Asn Ile  
 420 425 430  
 Arg Gly Tyr Asn Phe Asp Met Phe Ser Gly Val Lys Tyr Gln Val Asp  
 435 440 445  
 Val Thr Lys Pro Ala Gly Gln Arg Ile Ile Asn Pro Thr Ile Asn Asn  
 450 455 460  
 Lys Pro Ile Asp Pro Lys Ala Ile Tyr Lys Leu Ala Ile Asn Asn Tyr  
 465 470 475 480  
 Arg Phe Gly Thr Leu Ser Thr Thr Leu Asn Leu Val Thr Asp Ala Xaa  
 485 490 495  
 Arg Tyr Tyr Asn Ser Tyr Asp Glu Leu Gln Asp Asn Gly Gln Ile Arg  
 500 505 510  
 Asp Leu Ile Ile Lys Tyr Ile Thr Glu Glu Lys Gly Gly Lys Val Thr  
 515 520 525  
 Pro Glu Leu Glu Gly Asn Trp Glu Ile Ile Asn Tyr Asp Phe Lys Asn  
 530 535 540  
 Pro Leu Leu Glu Lys Leu Arg Glu Lys Leu Lys Glu Gly Ser Ile Lys  
 545 550 555 560  
 Ile Pro Thr Ser Lys Asp Gly Arg Thr Leu Asn Val Lys Ser Ile Lys  
 565 570 575  
 Glu Ser Glu Val Lys  
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<210> 73  
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 <212> DNA  
 <213> *Helicobacter pylori*

<220>  
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 <222> (68)...(1252)

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 gttggta atg gaa tca gta aaa aca gga aaa aca aat aag gtt ggc aag 109  
 Met Glu Ser Val Lys Thr Gly Lys Thr Asn Lys Val Gly Lys  
 1 5 10  
  
 aat aca gag atg gct aat aca aag gca aat aaa gag gct cat ttt aaa 157  
 Asn Thr Glu Met Ala Asn Thr Lys Ala Asn Lys Glu Ala His Phe Lys  
 15 20 25 30  
  
 caa gcg agc acc att aca aat ata atc aga tca att cgt ggg att ttt 205  
 Gln Ala Ser Thr Ile Thr Asn Ile Ile Arg Ser Ile Arg Gly Ile Phe

35										40					45					
aca	aaa	att	gca	aag	aaa	gtt	aga	gga	ctt	gta	aaa	aaa	cac	ccc	aag	253				
Thr	Lys	Ile	Ala	Lys	Lys	Val	Arg	Gly	Leu	Val	Lys	Lys	His	Pro	Lys					
50					55					60										
aaa	agc	agt	gcg	gca	tta	gta	gta	ttg	acc	cat	att	gcg	tgc	aag	aaa	301				
Lys	Ser	Ser	Ala	Ala	Leu	Val	Val	Leu	Thr	His	Ile	Ala	Cys	Lys	Lys					
65					70					75										
gcg	aaa	gaa	tta	gac	gat	aaa	gtc	caa	gat	aaa	tcc	aaa	caa	gct	gaa	349				
Ala	Lys	Glu	Leu	Asp	Asp	Lys	Val	Gln	Asp	Lys	Ser	Lys	Gln	Ala	Glu					
80					85					90										
aaa	gaa	aat	caa	atc	aat	tggt	tggt	aaa	tat	tca	gga	tta	aca	ata	gcg	397				
Lys	Glu	Asn	Gln	Ile	Asn	Trp	Trp	Lys	Tyr	Ser	Gly	Leu	Thr	Ile	Ala					
95					100					105					110					
aca	agt	tta	tta	tta	gcc	gct	tgt	agc	act	ggt	gat	gtt	agt	gaa	caa	445				
Thr	Ser	Leu	Leu	Leu	Ala	Ala	Cys	Ser	Thr	Gly	Asp	Val	Ser	Glu	Gln					
115					120					125										
ata	gaa	cta	gaa	caa	gaa	aaa	caa	aag	acg	agc	aat	ata	gag	act	aac	493				
Ile	Glu	Leu	Glu	Gln	Glu	Lys	Gln	Lys	Thr	Ser	Asn	Ile	Glu	Thr	Asn					
130					135					140										
aat	caa	ata	aaa	gta	gaa	caa	gaa	aaa	caa	aag	aca	agc	aat	ata	gag	541				
Asn	Gln	Ile	Lys	Val	Glu	Gln	Glu	Lys	Gln	Lys	Thr	Ser	Asn	Ile	Glu					
145					150					155										
act	aat	aat	caa	ata	aaa	gta	gaa	caa	gaa	caa	caa	aag	aca	agc	aat	589				
Thr	Asn	Asn	Gln	Ile	Lys	Val	Glu	Gln	Glu	Gln	Gln	Lys	Thr	Ser	Asn					
160					165					170										
aca	cag	aaa	gat	ttg	gtt	aaa	gaa	cag	aaa	gat	ttg	gtt	aaa	gaa	cag	637				
Thr	Gln	Lys	Asp	Leu	Val	Lys	Glu	Gln	Lys	Asp	Leu	Val	Lys	Glu	Gln					
175					180					185					190					
aaa	gat	ttg	gtt	aaa	gaa	cag	aaa	gat	ttg	gtt	aaa	gaa	cag	aaa	gat	685				
Lys	Asp	Leu	Val	Lys	Glu	Gln	Lys	Asp	Leu	Val	Lys	Glu	Gln	Lys	Asp					
195					200					205										
ttg	gtt	aaa	aca	cag	aaa	gat	ttc	att	aaa	tat	gta	gaa	caa	aat	tgc	733				
Leu	Val	Lys	Thr	Gln	Lys	Asp	Phe	Ile	Lys	Tyr	Val	Glu	Gln	Asn	Cys					
210					215					220										
caa	gaa	aat	cat	aat	caa	ttc	ttt	att	gaa	aaa	gga	gga	att	aag	gct	781				
Gln	Glu	Asn	His	Asn	Gln	Phe	Phe	Ile	Glu	Lys	Gly	Gly	Ile	Lys	Ala					
225					230					235										
ggt	att	ggt	ata	gaa	gta	gaa	gct	gaa	tgc	aaa	acc	cct	aaa	cct	gca	829				
Gly	Ile	Gly	Ile	Glu	Val	Glu	Ala	Glu	Cys	Lys	Thr	Pro	Lys	Pro	Ala					
240					245					250										
aaa	acc	aat	caa	acc	cct	atc	cag	cca	aaa	cac	ctc	cca	aac	tct	aaa	877				
Lys	Thr	Asn	Gln	Thr	Pro	Ile	Gln	Pro	Lys	His	Leu	Pro	Asn	Ser	Lys					
255					260					265					270					
caa	ccc	cg	tct	caa	aga	gga	tca	aaa	gcg	caa	gag	ctt	atc	gct	tat	925				



Gln	Pro	Arg	Ser	Gln	Arg	Gly	Ser	Lys	Ala	Gln	Glu	Leu	Ile	Ala	Tyr	
				275					280					285		
ttg	caa	aaa	gag	cta	gaa	ttt	ctg	ccc	tat	tcg	caa	aaa	gct	atc	gct	973
Leu	Gln	Lys	Glu	Leu	Glu	Phe	Leu	Pro	Tyr	Ser	Gln	Lys	Ala	Ile	Ala	
			290					295					300			
aaa	caa	gtg	gat	ttt	tac	agg	cca	agt	tct	atc	gct	tat	tta	gaa	cta	1021
Lys	Gln	Val	Asp	Phe	Tyr	Arg	Pro	Ser	Ser	Ile	Ala	Tyr	Leu	Glu	Leu	
		305					310					315				
gat	cct	aga	gat	ttt	aag	ggt	aca	gaa	gaa	tgg	caa	aaa	gaa	aat	cta	1069
Asp	Pro	Arg	Asp	Phe	Lys	Val	Thr	Glu	Glu	Trp	Gln	Lys	Glu	Asn	Leu	
	320					325					330					
aaa	ata	cgc	tct	aaa	gct	caa	gct	aaa	atg	ctt	gaa	atg	aga	aac	cca	1117
Lys	Ile	Arg	Ser	Lys	Ala	Gln	Ala	Lys	Met	Leu	Glu	Met	Arg	Asn	Pro	
335				340						345					350	
caa	gcc	cac	ctt	tca	aac	tct	caa	agc	ctt	ttg	ttc	ggt	caa	aaa	ata	1165
Gln	Ala	His	Leu	Ser	Asn	Ser	Gln	Ser	Leu	Leu	Phe	Val	Gln	Lys	Ile	
			355					360					365			
ttt	gct	gat	ggt	aat	aaa	gaa	ata	gaa	gca	ggt	gct	aat	act	gaa	aag	1213
Phe	Ala	Asp	Val	Asn	Lys	Glu	Ile	Glu	Ala	Val	Ala	Asn	Thr	Glu	Lys	
			370					375					380			
aaa	gca	gaa	aaa	gcg	ggt	tat	ggt	tat	agt	aaa	agg	atg	tagcgggtaa			1262
Lys	Ala	Glu	Lys	Ala	Gly	Tyr	Gly	Tyr	Ser	Lys	Arg	Met				
	385				390						395					
aaacattgca	ccaagttttt	aattatctgt	cggtttttga	aaacattttt	tatggtagcg											1322
ttatttggca	ataaaaag															1339

<210> 74  
 <211> 395  
 <212> PRT  
 <213> Helicobacter pylori

<400> 74  
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 20 25 30  
 Ser Thr Ile Thr Asn Ile Ile Arg Ser Ile Arg Gly Ile Phe Thr Lys  
 35 40 45  
 Ile Ala Lys Lys Val Arg Gly Leu Val Lys Lys His Pro Lys Lys Ser  
 50 55 60  
 Ser Ala Ala Leu Val Val Leu Thr His Ile Ala Cys Lys Lys Ala Lys  
 65 70 75 80  
 Glu Leu Asp Asp Lys Val Gln Asp Lys Ser Lys Gln Ala Glu Lys Glu  
 85 90 95  
 Asn Gln Ile Asn Trp Trp Lys Tyr Ser Gly Leu Thr Ile Ala Thr Ser  
 100 105 110  
 Leu Leu Leu Ala Ala Cys Ser Thr Gly Asp Val Ser Glu Gln Ile Glu  
 115 120 125  
 Leu Glu Gln Glu Lys Gln Lys Thr Ser Asn Ile Glu Thr Asn Asn Gln  
 130 135 140  
 Ile Lys Val Glu Gln Glu Lys Gln Lys Thr Ser Asn Ile Glu Thr Asn

145	Asn	Gln	Ile	Lys	Val	150	Glu	Gln	Glu	Gln	155	Lys	Thr	Ser	Asn	Thr	160	Gln
					165						170						175	
	Lys	Asp	Leu	Val	Lys	Glu	Gln	Lys	Asp	Leu	Val	Lys	Glu	Gln	Lys	Asp		
				180					185						190			
	Leu	Val	Lys	Glu	Gln	Lys	Asp	Leu	Val	Lys	Glu	Gln	Lys	Asp	Leu	Val		
		195						200					205					
	Lys	Thr	Gln	Lys	Asp	Phe	Ile	Lys	Tyr	Val	Glu	Gln	Asn	Cys	Gln	Glu		
		210					215						220					
	Asn	His	Asn	Gln	Phe	Phe	Ile	Glu	Lys	Gly	Gly	Ile	Lys	Ala	Gly	Ile		
	225					230					235					240		
	Gly	Ile	Glu	Val	Glu	Ala	Glu	Cys	Lys	Thr	Pro	Lys	Pro	Ala	Lys	Thr		
				245						250					255			
	Asn	Gln	Thr	Pro	Ile	Gln	Pro	Lys	His	Leu	Pro	Asn	Ser	Lys	Gln	Pro		
			260						265					270				
	Arg	Ser	Gln	Arg	Gly	Ser	Lys	Ala	Gln	Glu	Leu	Ile	Ala	Tyr	Leu	Gln		
		275						280					285					
	Lys	Glu	Leu	Glu	Phe	Leu	Pro	Tyr	Ser	Gln	Lys	Ala	Ile	Ala	Lys	Gln		
		290					295					300						
	Val	Asp	Phe	Tyr	Arg	Pro	Ser	Ser	Ile	Ala	Tyr	Leu	Glu	Leu	Asp	Pro		
	305					310					315				320			
	Arg	Asp	Phe	Lys	Val	Thr	Glu	Glu	Trp	Gln	Lys	Glu	Asn	Leu	Lys	Ile		
				325						330					335			
	Arg	Ser	Lys	Ala	Gln	Ala	Lys	Met	Leu	Glu	Met	Arg	Asn	Pro	Gln	Ala		
			340						345					350				
	His	Leu	Ser	Asn	Ser	Gln	Ser	Leu	Phe	Val	Gln	Lys	Ile	Phe	Ala			
		355					360					365						
	Asp	Val	Asn	Lys	Glu	Ile	Glu	Ala	Val	Ala	Asn	Thr	Glu	Lys	Lys	Ala		
		370				375						380						
	Glu	Lys	Ala	Gly	Tyr	Gly	Tyr	Ser	Lys	Arg	Met							
	385					390					395							

<210> 75  
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 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (70)...(864)

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 aggttaaac atg att aaa caa acc ctc atc att ctt gcc cct ttt ttt atc 111  
 Met Ile Lys Gln Thr Leu Ile Ile Leu Ala Pro Phe Phe Ile  
 1 5 10

gca acg ctg ttg tat ttt tta ggc gca ccg gat ggg tta aga cct aac 159  
 Ala Thr Leu Leu Tyr Phe Leu Gly Ala Pro Asp Gly Leu Arg Pro Asn  
 15 20 25 30

gct tgg ctt tat ttt tgt att ttc atg ggc atg att ata ggg cta att 207  
 Ala Trp Leu Tyr Phe Cys Ile Phe Met Gly Met Ile Ile Gly Leu Ile  
 35 40 45

tta gag ccg gtg cca tca ggt tta ata gcg cta agc gcg tta gtg ctg 255  
 Leu Glu Pro Val Pro Ser Gly Leu Ile Ala Leu Ser Ala Leu Val Leu  
 50 55 60

tgt ata gcg tta aaa att gga gcg agc gat aaa gta gcg agc gct aat	303
Cys Ile Ala Leu Lys Ile Gly Ala Ser Asp Lys Val Ala Ser Ala Asn	
65 70 75	
aag gct att tcg tgg ggt ttg agc ggg tat gcg aat aaa acg gtg tgg	351
Lys Ala Ile Ser Trp Gly Leu Ser Gly Tyr Ala Asn Lys Thr Val Trp	
80 85 90	
ctt gtg ttt gtc gct ttc att ttg ggt tta ggg tat gaa aaa agc ttg	399
Leu Val Phe Val Ala Phe Ile Leu Gly Leu Gly Tyr Glu Lys Ser Leu	
95 100 105 110	
tta ggg aaa cgg atc gct ctt tta ctg att agg ttt tta ggg caa acc	447
Leu Gly Lys Arg Ile Ala Leu Leu Leu Ile Arg Phe Leu Gly Gln Thr	
115 120 125	
cct tta ggt tta ggc tat gcg att ggt ttg agc gaa ttg tgt cta gcc	495
Pro Leu Gly Leu Gly Tyr Ala Ile Gly Leu Ser Glu Leu Cys Leu Ala	
130 135 140	
cct ttt atc cct agc aac tcc gct aga agt gga ggc ata ctc tat ccc	543
Pro Phe Ile Pro Ser Asn Ser Ala Arg Ser Gly Gly Ile Leu Tyr Pro	
145 150 155	
atc gtt tca tct atc ccg cct tta atg gga tct act cca aat aat aac	591
Ile Val Ser Ser Ile Pro Pro Leu Met Gly Ser Thr Pro Asn Asn Asn	
160 165 170	
cct gac aaa atc ggc gcg tat ttg atg tgg gtc gct ttg gct tca act	639
Pro Asp Lys Ile Gly Ala Tyr Leu Met Trp Val Ala Leu Ala Ser Thr	
175 180 185 190	
tgc atc act tcg tcc atg ttt tta acc gcg ctc gct cct aac ccc cta	687
Cys Ile Thr Ser Ser Met Phe Leu Thr Ala Leu Ala Pro Asn Pro Leu	
195 200 205	
gca atg gaa atc gct gcc aaa atg ggc gtg aat gaa atc tca tgg ttt	735
Ala Met Glu Ile Ala Ala Lys Met Gly Val Asn Glu Ile Ser Trp Phe	
210 215 220	
tcg tgg ttt tta gcg ttc ttg cct tgt ggg gtg gtt ttg atc ttg ctt	783
Ser Trp Phe Leu Ala Phe Leu Pro Cys Gly Val Val Leu Ile Leu Leu	
225 230 235	
gtg cct tta ttg gcg tat aaa acc tgc aaa ccc acc tta aaa ggc tca	831
Val Pro Leu Leu Ala Tyr Lys Thr Cys Lys Pro Thr Leu Lys Gly Ser	
240 245 250	
aaa gaa gtg agt ttg tgg gcc aaa aaa agg aat tagaggcat ggggaggttt	884
Lys Glu Val Ser Leu Trp Ala Lys Lys Arg Asn	
255 260 265	
tctttaaaag aaattttaat	904

<210> 76  
 <211> 265  
 <212> PRT  
 <213> Helicobacter pylori

<400> 76

Met	Ile	Lys	Gln	Thr	Leu	Ile	Ile	Leu	Ala	Pro	Phe	Phe	Ile	Ala	Thr
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		20						25					30		
Leu	Tyr	Phe	Cys	Ile	Phe	Met	Gly	Met	Ile	Ile	Gly	Leu	Ile	Leu	Glu
	35						40					45			
Pro	Val	Pro	Ser	Gly	Leu	Ile	Ala	Leu	Ser	Ala	Leu	Val	Leu	Cys	Ile
	50					55					60				
Ala	Leu	Lys	Ile	Gly	Ala	Ser	Asp	Lys	Val	Ala	Ser	Ala	Asn	Lys	Ala
65					70					75					80
Ile	Ser	Trp	Gly	Leu	Ser	Gly	Tyr	Ala	Asn	Lys	Thr	Val	Trp	Leu	Val
			85						90					95	
Phe	Val	Ala	Phe	Ile	Leu	Gly	Leu	Gly	Tyr	Glu	Lys	Ser	Leu	Leu	Gly
		100						105					110		
Lys	Arg	Ile	Ala	Leu	Leu	Leu	Ile	Arg	Phe	Leu	Gly	Gln	Thr	Pro	Leu
		115					120					125			
Gly	Leu	Gly	Tyr	Ala	Ile	Gly	Leu	Ser	Glu	Leu	Cys	Leu	Ala	Pro	Phe
	130					135					140				
Ile	Pro	Ser	Asn	Ser	Ala	Arg	Ser	Gly	Gly	Ile	Leu	Tyr	Pro	Ile	Val
145					150					155					160
Ser	Ser	Ile	Pro	Pro	Leu	Met	Gly	Ser	Thr	Pro	Asn	Asn	Asn	Pro	Asp
			165						170					175	
Lys	Ile	Gly	Ala	Tyr	Leu	Met	Trp	Val	Ala	Leu	Ala	Ser	Thr	Cys	Ile
		180						185					190		
Thr	Ser	Ser	Met	Phe	Leu	Thr	Ala	Leu	Ala	Pro	Asn	Pro	Leu	Ala	Met
		195					200					205			
Glu	Ile	Ala	Ala	Lys	Met	Gly	Val	Asn	Glu	Ile	Ser	Trp	Phe	Ser	Trp
	210					215					220				
Phe	Leu	Ala	Phe	Leu	Pro	Cys	Gly	Val	Val	Leu	Ile	Leu	Leu	Val	Pro
225					230					235					240
Leu	Leu	Ala	Tyr	Lys	Thr	Cys	Lys	Pro	Thr	Leu	Lys	Gly	Ser	Lys	Glu
			245						250					255	
Val	Ser	Leu	Trp	Ala	Lys	Lys	Arg	Asn							
		260						265							

<210> 77  
 <211> 1194  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (152)...(1069)

<400> 77

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tgagcttttg	cttagttttg	taaggaatga	g atg ata aag agt tgg act aaa			172
			Met Ile Lys Ser Trp Thr Lys			
			1	5		
aag tgg ttt ttg att tta ttt tta atg gca agt tgt tcc agt tat ttg						220
Lys Trp Phe Leu Ile Leu Phe Leu Met Ala Ser Cys Ser Ser Tyr Leu						
	10		15		20	
gtg gct aca acc ggt gag aaa tat ttt aaa atg gct act caa gcc ttt						268
Val Ala Thr Thr Gly Glu Lys Tyr Phe Lys Met Ala Thr Gln Ala Phe						

25	30	35	
aag aga ggg gac tac cat Lys Arg Gly Asp Tyr His 40	aaa gcg gtg gct Lys Ala Val Ala 45	ttt tat aag agg agc tgt Phe Tyr Lys Arg Ser Cys 50	316
aat tta agg gtg ggg gtt ggt tgc acg agt Asn Leu Arg Val Gly Val Gly Cys Thr Ser 60	ttt ggc tct atg tat gaa Leu Gly Ser Met Tyr Glu 65		364
gat ggc gat ggc gtg gat cag aat att aca aaa gcc gtt ttt tat tac Asp Gly Asp Gly Val Asp Gln Asn Ile Thr Lys Ala Val Phe Tyr Tyr 75			412
aga aga ggg tgt aat tta agg aat cat ctc gct tgc gcg agt cta ggc Arg Arg Gly Cys Asn Leu Arg Asn His Leu Ala Cys Ala Ser Leu Gly 90			460
tct atg tat gaa gat ggc gat ggt gtg caa aaa aac ctt cca aag gct Ser Met Tyr Glu Asp Gly Asp Gly Val Gln Lys Asn Leu Pro Lys Ala 105			508
atc tat tat tac agg aga ggg tgc cac tta aag ggt ggg gtg agc tgt Ile Tyr Tyr Tyr Arg Gly Cys His Leu Lys Gly Gly Val Ser Cys 120			556
ggg agt tta ggt ttt atg tat ttt aat ggc acg ggc gtt aag caa aat Gly Ser Leu Gly Phe Met Tyr Phe Asn Gly Thr Gly Val Lys Gln Asn 140			604
tat gcc aaa gcc ctt ttt ctt tct aaa tac gct tgc agt ttg aat tac Tyr Ala Lys Ala Leu Phe Leu Ser Lys Tyr Ala Cys Ser Leu Asn Tyr 155			652
ggc att agt tgt aac ttt gta ggg tat atg tat agg aac gcc aaa ggc Gly Ile Ser Cys Asn Phe Val Gly Tyr Met Tyr Arg Asn Ala Lys Gly 170			700
gta cag aag gat ttg aaa aaa gcc ctt gcg aat ttt aaa aga ggg tgc Val Gln Lys Asp Leu Lys Lys Ala Leu Ala Asn Phe Lys Arg Gly Cys 185			748
cat ttg aaa gac gga gcg agt tgt gtg agc ttg gga tac atg tat gaa His Leu Lys Asp Gly Ala Ser Cys Val Ser Leu Gly Tyr Met Tyr Glu 200			796
gtc ggt atg gat gtc aaa caa aat gga gag caa gcc ttg aat ctt tat Val Gly Met Asp Val Lys Gln Asn Gly Glu Gln Ala Leu Asn Leu Tyr 220			844
aaa aag ggt tgt tat tta aaa agg ggg agc ggt tgt cat aat gtg gcg Lys Lys Gly Cys Tyr Leu Lys Arg Gly Ser Gly Cys His Asn Val Ala 235			892
gtg atg tat tac acc ggt aag ggc gtt cca aag gat tta gat aaa gcc Val Met Tyr Tyr Thr Gly Lys Gly Val Pro Lys Asp Leu Asp Lys Ala 250			940
att tcg tat tat aag aaa ggt tgc act cta ggc ttt agt ggt agc tgt			988

Ile Ser Tyr Tyr Lys Lys Gly Cys Thr Leu Gly Phe Ser Gly Ser Cys  
 265 270 275  
 aaa gtg tta gaa gaa gtg att ggc aag aag tct gat gat ttg caa gat 1036  
 Lys Val Leu Glu Glu Val Ile Gly Lys Lys Ser Asp Asp Leu Gln Asp  
 280 285 290 295  
 gac gcg caa aac gac acg caa gat gat atg caa taagttaaag cttatggact 1089  
 Asp Ala Gln Asn Asp Thr Gln Asp Asp Met Gln  
 300 305  
 aatgattaaa actcatctta tagaaatctt tctactctct tggtatcaaa tagggattaa 1149  
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 <213> Helicobacter pylori  
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 Lys Met Ala Thr Gln Ala Phe Lys Arg Gly Asp Tyr His Lys Ala Val  
 35 40 45  
 Ala Phe Tyr Lys Arg Ser Cys Asn Leu Arg Val Gly Val Gly Cys Thr  
 50 55 60  
 Ser Leu Gly Ser Met Tyr Glu Asp Gly Asp Gly Val Asp Gln Asn Ile  
 65 70 75 80  
 Thr Lys Ala Val Phe Tyr Tyr Arg Arg Gly Cys Asn Leu Arg Asn His  
 85 90 95  
 Leu Ala Cys Ala Ser Leu Gly Ser Met Tyr Glu Asp Gly Asp Gly Val  
 100 105 110  
 Gln Lys Asn Leu Pro Lys Ala Ile Tyr Tyr Tyr Arg Arg Gly Cys His  
 115 120 125  
 Leu Lys Gly Gly Val Ser Cys Gly Ser Leu Gly Phe Met Tyr Phe Asn  
 130 135 140  
 Gly Thr Gly Val Lys Gln Asn Tyr Ala Lys Ala Leu Phe Leu Ser Lys  
 145 150 155 160  
 Tyr Ala Cys Ser Leu Asn Tyr Gly Ile Ser Cys Asn Phe Val Gly Tyr  
 165 170 175  
 Met Tyr Arg Asn Ala Lys Gly Val Gln Lys Asp Leu Lys Lys Ala Leu  
 180 185 190  
 Ala Asn Phe Lys Arg Gly Cys His Leu Lys Asp Gly Ala Ser Cys Val  
 195 200 205  
 Ser Leu Gly Tyr Met Tyr Glu Val Gly Met Asp Val Lys Gln Asn Gly  
 210 215 220  
 Glu Gln Ala Leu Asn Leu Tyr Lys Lys Gly Cys Tyr Leu Lys Arg Gly  
 225 230 235 240  
 Ser Gly Cys His Asn Val Ala Val Met Tyr Tyr Thr Gly Lys Gly Val  
 245 250 255  
 Pro Lys Asp Leu Asp Lys Ala Ile Ser Tyr Tyr Lys Lys Gly Cys Thr  
 260 265 270  
 Leu Gly Phe Ser Gly Ser Cys Lys Val Leu Glu Glu Val Ile Gly Lys  
 275 280 285  
 Lys Ser Asp Asp Leu Gln Asp Asp Ala Gln Asn Asp Thr Gln Asp Asp  
 290 295 300  
 Met Gln

[illegible]

Gln Asn Phe Trp Leu Leu Tyr Ile Phe Leu Leu Phe Ala Val Glu Leu  
 170 175 180  
 cat ggc tct att ggg ttg tat cgt tta gcg atc aaa tgg ggg tgg ttt 691  
 His Gly Ser Ile Gly Leu Tyr Arg Leu Ala Ile Lys Trp Gly Trp Phe  
 185 190 195  
 aaa aat gtg agc att caa ggt ttg aga aaa gtc aaa tgg gcg atg agc 739  
 Lys Asn Val Ser Ile Gln Gly Leu Arg Lys Val Lys Trp Ala Met Ser  
 200 205 210  
 gtg ttt ttt att gtt tta ggg ctt tgc acc tat ggg gct tac att aaa 787  
 Val Phe Phe Ile Val Leu Gly Leu Cys Thr Tyr Gly Ala Tyr Ile Lys  
 215 220 225  
 aaa ggt tta gaa aat aag gaa aat ggc att aaa acc atg caa gaa gcc 835  
 Lys Gly Leu Glu Asn Lys Glu Asn Gly Ile Lys Thr Met Gln Glu Ala  
 230 235 240 245  
 ata gaa gct gat ggg aaa ttc cac aaa gaa taagggtaga aaatgaaaat 885  
 Ile Glu Ala Asp Gly Lys Phe His Lys Glu  
 250 255  
 aacatattgt gatgcgctaa ttattggagg cggactagct gggttaaggg ctagtatcgc 945  
 atgcaaaca aagggtttta acaccatcgt ttttaagccta gtgcctgtca ggcggt 1001

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 <211> 255  
 <212> PRT  
 <213> Helicobacter pylori

<400> 80  
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 Leu Lys Lys Ser Gly Ile Tyr Ala Lys Leu Asp Phe Leu Gln Ser Ala  
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 Thr Gly Leu Ile Leu Ala Leu Phe Met Ile Ala His Met Phe Leu Val  
 35 40 45  
 Ser Ser Ile Leu Ile Ser Asp Glu Ala Met Tyr Lys Val Ala Lys Phe  
 50 55 60  
 Phe Glu Gly Ser Leu Phe Leu Lys Ala Gly Glu Pro Ala Ile Val Ser  
 65 70 75 80  
 Val Val Ala Ala Gly Ile Ile Leu Ile Leu Val Ala His Ala Phe Leu  
 85 90 95  
 Ala Leu Arg Lys Phe Pro Ile Asn Tyr Arg Gln Tyr Lys Val Phe Lys  
 100 105 110  
 Thr His Lys His Leu Met Lys His Gly Asp Thr Ser Leu Trp Phe Ile  
 115 120 125  
 Gln Ala Leu Thr Gly Phe Ala Met Phe Phe Leu Ala Ser Ile His Leu  
 130 135 140  
 Phe Val Met Leu Thr Glu Pro Glu Ser Ile Gly Pro His Gly Ser Ser  
 145 150 155 160  
 Tyr Arg Phe Val Thr Gln Asn Phe Trp Leu Leu Tyr Ile Phe Leu Leu  
 165 170 175  
 Phe Ala Val Glu Leu His Gly Ser Ile Gly Leu Tyr Arg Leu Ala Ile  
 180 185 190  
 Lys Trp Gly Trp Phe Lys Asn Val Ser Ile Gln Gly Leu Arg Lys Val  
 195 200 205  
 Lys Trp Ala Met Ser Val Phe Phe Ile Val Leu Gly Leu Cys Thr Tyr



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		Met	Glu Glu Ser	Thr	Ala Phe Ile	Leu Ala										
		1		5		10										
ctt gtg ggg cta ttc acc ggc att acc gcc ggg ttt ttt ggt att ggt	159															
Leu Val Gly Leu Phe Thr Gly Ile Thr Ala Gly Phe Phe Gly Ile Gly																
			15				20						25			
ggg ggg gag att gtc gtc cct agc gcg att ttt gcc cat ttt agc tat	207															
Gly Gly Glu Ile Val Val Pro Ser Ala Ile Phe Ala His Phe Ser Tyr																
			30				35						40			
agc cat gcg gtg ggt att tcg ctc atg caa atg ctt ttt tct tca gtg	255															
Ser His Ala Val Gly Ile Ser Leu Met Gln Met Leu Phe Ser Ser Val																
		45				50					55					
gtc ggc tct atc atc aat tac aaa aag ggc tta ttg gat ttg aga gaa	303															
Val Gly Ser Ile Ile Asn Tyr Lys Lys Gly Leu Leu Asp Leu Arg Glu																
		60				65					70					
ggc tca ttt gcc gcg ctt gga ggg cta atg gga gcg att tta ggg agc	351															
Gly Ser Phe Ala Ala Leu Gly Gly Leu Met Gly Ala Ile Leu Gly Ser																
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ttt atc tta aaa atc att gac gat aaa att tta atg gcg gtg ttt gtg	399															
Phe Ile Leu Lys Ile Ile Asp Asp Lys Ile Leu Met Ala Val Phe Val																
				95				100						105		
gtg gtg gtg tgc tac acc ttt atc aaa tac gct ttt tct agc aac aag	447															
Val Val Val Cys Tyr Thr Phe Ile Lys Tyr Ala Phe Ser Ser Asn Lys																
			110				115						120			
aaa ccc aag cat ttt gaa gaa atg cat ttt gat ttg cat gcg aat aac	495															
Lys Pro Lys His Phe Glu Glu Met His Phe Asp Leu His Ala Asn Asn																
		125				130					135					
aaa acg ccc gaa aaa aag cgc gca atc cct ttt gtg tct atg gat aga	543															
Lys Thr Pro Glu Lys Lys Arg Ala Ile Pro Phe Val Ser Met Asp Arg																
		140				145					150					
acg cat ggg gtt ttg atg ctc gcc ggt ttt gtt acc ggc atc ttt tct	591															

Thr	His	Gly	Val	Leu	Met	Leu	Ala	Gly	Phe	Val	Thr	Gly	Ile	Phe	Ser		
155					160					165					170		
atc	cca	cta	ggc	atg	ggg	gga	ggg	att	tta	atg	gtg	ccg	ttt	ttg	ggc	639	
Ile	Pro	Leu	Gly	Met	Gly	Gly	Gly	Ile	Leu	Met	Val	Pro	Phe	Leu	Gly		
				175				180						185			
tat	ttt	ttg	aaa	tac	gat	tct	aaa	aaa	atc	gtg	cct	ttg	ggg	cta	ttt	687	
Tyr	Phe	Leu	Lys	Tyr	Asp	Ser	Lys	Lys	Ile	Val	Pro	Leu	Gly	Leu	Phe		
			190				195						200				
ttt	gtg	gtg	ttc	gct	tct	tta	tct	ggg	gtc	atc	tct	ctt	tat	aac	ggg	735	
Phe	Val	Val	Phe	Ala	Ser	Leu	Ser	Gly	Val	Ile	Ser	Leu	Tyr	Asn	Gly		
		205					210					215					
agg	gtt	ctt	gat	aat	ata	agc	gtt	caa	gcg	ggg	gtg	att	acc	ggc	att	783	
Arg	Val	Leu	Asp	Asn	Ile	Ser	Val	Gln	Ala	Gly	Val	Ile	Thr	Gly	Ile		
	220					225					230						
gga	gcg	ttt	tta	ggc	gtg	ggc	att	ggc	atc	aag	ctt	atc	gct	ttg	gct	831	
Gly	Ala	Phe	Leu	Gly	Val	Gly	Ile	Gly	Ile	Lys	Leu	Ile	Ala	Leu	Ala		
235				240					245					250			
aat	gaa	aag	gtg	cat	aaa	atc	ctg	ttg	ctc	ctt	att	tat	gct	tta	agc	879	
Asn	Glu	Lys	Val	His	Lys	Ile	Leu	Leu	Leu	Leu	Ile	Tyr	Ala	Leu	Ser		
				255				260						265			
att	tta	gcg	act	tta	cac	aag	ctc	att	atg	ggg	taa	atc	taaa	aac	gcttcta	932	
Ile	Leu	Ala	Thr	Leu	His	Lys	Leu	Ile	Met	Gly							
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 <212> PRT  
 <213> Helicobacter pylori

<400> 82

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			20				25						30				
Pro	Ser	Ala	Ile	Phe	Ala	His	Phe	Ser	Tyr	Ser	His	Ala	Val	Gly	Ile		
		35				40					45						
Ser	Leu	Met	Gln	Met	Leu	Phe	Ser	Ser	Val	Val	Gly	Ser	Ile	Ile	Asn		
	50			55				60									
Tyr	Lys	Lys	Gly	Leu	Leu	Asp	Leu	Arg	Glu	Gly	Ser	Phe	Ala	Ala	Leu		
65				70				75						80			
Gly	Gly	Leu	Met	Gly	Ala	Ile	Leu	Gly	Ser	Phe	Ile	Leu	Lys	Ile	Ile		
			85				90						95				
Asp	Asp	Lys	Ile	Leu	Met	Ala	Val	Phe	Val	Val	Val	Val	Cys	Tyr	Thr		
			100			105							110				
Phe	Ile	Lys	Tyr	Ala	Phe	Ser	Ser	Asn	Lys	Lys	Pro	Lys	His	Phe	Glu		
		115				120					125						
Glu	Met	His	Phe	Asp	Leu	His	Ala	Asn	Asn	Lys	Thr	Pro	Glu	Lys	Lys		
	130				135						140						
Arg	Ala	Ile	Pro	Phe	Val	Ser	Met	Asp	Arg	Thr	His	Gly	Val	Leu	Met		
145				150						155					160		

Leu Ala Gly Phe Val Thr Gly Ile Phe Ser Ile Pro Leu Gly Met Gly  
 165 170 175  
 Gly Gly Ile Leu Met Val Pro Phe Leu Gly Tyr Phe Leu Lys Tyr Asp  
 180 185 190  
 Ser Lys Lys Ile Val Pro Leu Gly Leu Phe Phe Val Val Phe Ala Ser  
 195 200 205  
 Leu Ser Gly Val Ile Ser Leu Tyr Asn Gly Arg Val Leu Asp Asn Ile  
 210 215 220  
 Ser Val Gln Ala Gly Val Ile Thr Gly Ile Gly Ala Phe Leu Gly Val  
 225 230 235 240  
 Gly Ile Gly Ile Lys Leu Ile Ala Leu Ala Asn Glu Lys Val His Lys  
 245 250 255  
 Ile Leu Leu Leu Leu Ile Tyr Ala Leu Ser Ile Leu Ala Thr Leu His  
 260 265 270  
 Lys Leu Ile Met Gly  
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<210> 83  
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 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (220)...(1482)

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 ttatagtcaa taccacgcgc tcaaaaaagg gcttttaaaa acgctctgct ttttagcctt 180  
 cctttaagcg tggcgtttagc tgaagacgat ggcttttat atg gga gtg ggc tat 234  
 Met Gly Val Gly Tyr  
 1 5  
  
 caa atc ggc ggc gcg caa caa aat atc gat aac aaa ggc agc acc cta 282  
 Gln Ile Gly Gly Ala Gln Gln Asn Ile Asp Asn Lys Gly Ser Thr Leu  
 10 15 20  
  
 agg aat aat gtc att aat aat ttc cgc caa gtg ggc gtg ggt atg gca 330  
 Arg Asn Asn Val Ile Asn Asn Phe Arg Gln Val Gly Val Gly Met Ala  
 25 30 35  
  
 ggg ggt aat ggg ctt tta gcc tta gcg aca aac acg acc atg gac gct 378  
 Gly Gly Asn Gly Leu Leu Ala Leu Ala Thr Asn Thr Thr Met Asp Ala  
 40 45 50  
  
 ctt tta ggg ata ggc aac caa att gtc aat act aat aca act gtt agc 426  
 Leu Leu Gly Ile Gly Asn Gln Ile Val Asn Thr Asn Thr Thr Val Ser  
 55 60 65  
  
 aac aac aac gca gaa tta acc cag ttt aaa aaa ata ctc cct caa att 474  
 Asn Asn Asn Ala Glu Leu Thr Gln Phe Lys Lys Ile Leu Pro Gln Ile  
 70 75 80 85  
  
 gag caa cgc ttt gaa acg aat aaa aac gct tat agc gtt caa gcc ttg 522  
 Glu Gln Arg Phe Glu Thr Asn Lys Asn Ala Tyr Ser Val Gln Ala Leu  
 90 95 100

caa gtg tat ttg agt aat gtg ctt tat aac ttg gtt aat aat agt aat	570
Gln Val Tyr Leu Ser Asn Val Leu Tyr Asn Leu Val Asn Asn Ser Asn	
105 110 115	
aat ggc agt aat aat gga gtc gtt cct gaa tat gta gga att ata aaa	618
Asn Gly Ser Asn Asn Gly Val Val Pro Glu Tyr Val Gly Ile Ile Lys	
120 125 130	
gtt ctc tat ggt tct caa aat gaa ttc agt ctc tta gcc acg gag agt	666
Val Leu Tyr Gly Ser Gln Asn Glu Phe Ser Leu Leu Ala Thr Glu Ser	
135 140 145	
gtg gtg ctt tta aac gcg ctt aca agg gtg aat ctg gat agt aat tcg	714
Val Val Leu Leu Asn Ala Leu Thr Arg Val Asn Leu Asp Ser Asn Ser	
150 155 160 165	
gtg ttt tta aaa ggg cta tta gcc caa atg cag ctt ttt aat gac act	762
Val Phe Leu Lys Gly Leu Leu Ala Gln Met Gln Leu Phe Asn Asp Thr	
170 175 180	
tct tca gca aag cta ggc cag atc gca gaa aac ttg aag aac ggt ggt	810
Ser Ser Ala Lys Leu Gly Gln Ile Ala Glu Asn Leu Lys Asn Gly Gly	
185 190 195	
gca gga tca atg ctc caa aag gat gtg aaa acc atc tcg gat cga atc	858
Ala Gly Ser Met Leu Gln Lys Asp Val Lys Thr Ile Ser Asp Arg Ile	
200 205 210	
gct act tac caa gag aat cta aaa cag cta gga ggg atg cta aag aat	906
Ala Thr Tyr Gln Glu Asn Leu Lys Gln Leu Gly Gly Met Leu Lys Asn	
215 220 225	
tac gat gaa ccc tac ttg ccc caa ttt ggg cca ggc aca agc tct cag	954
Tyr Asp Glu Pro Tyr Leu Pro Gln Phe Gly Pro Gly Thr Ser Ser Gln	
230 235 240 245	
cat ggg gtt att aat ggc ttt ggc att caa gtg ggc tat aag caa ttt	1002
His Gly Val Ile Asn Gly Phe Gly Ile Gln Val Gly Tyr Lys Gln Phe	
250 255 260	
ttt ggg aac aag cgg aat ata ggc tta cga tat tac gct ttc ttt gat	1050
Phe Gly Asn Lys Arg Asn Ile Gly Leu Arg Tyr Tyr Ala Phe Phe Asp	
265 270 275	
tat ggc ttt acg caa ttg ggc agt ctt agc agc gcc gtt aaa gcg aat	1098
Tyr Gly Phe Thr Gln Leu Gly Ser Leu Ser Ser Ala Val Lys Ala Asn	
280 285 290	
atc ttt act tat ggc gct ggc acg gac ttt tta tgg aat atc ttt aga	1146
Ile Phe Thr Tyr Gly Ala Gly Thr Asp Phe Leu Trp Asn Ile Phe Arg	
295 300 305	
agg gtt ttt agc gat cag tcc ttg aat gtg ggg gtg ttt ggg ggc att	1194
Arg Val Phe Ser Asp Gln Ser Leu Asn Val Gly Val Phe Gly Gly Ile	
310 315 320 325	
caa ata gcg ggt aac act tgg gat agc tct tta aga ggt caa att gaa	1242
Gln Ile Ala Gly Asn Thr Trp Asp Ser Ser Leu Arg Gly Gln Ile Glu	
330 335 340	

aac tcg ttt aaa gaa tac ccc act ccc acg aat ttc caa ttt ttg ttt 1290  
 Asn Ser Phe Lys Glu Tyr Pro Thr Pro Thr Asn Phe Gln Phe Leu Phe  
 345 350 355  
 aat ttg ggt tta agg gct cat ttt gcc agc acc atg cac cgc cgg ttt 1338  
 Asn Leu Gly Leu Arg Ala His Phe Ala Ser Thr Met His Arg Arg Phe  
 360 365 370  
 ttg agc gcg tct caa agc att cag cat ggg atg gaa ttt ggc gtg aaa 1386  
 Leu Ser Ala Ser Gln Ser Ile Gln His Gly Met Glu Phe Gly Val Lys  
 375 380 385  
 atc ccg gct atc aat caa agg tat ttg agg gcc aat ggg gct gat gtg 1434  
 Ile Pro Ala Ile Asn Gln Arg Tyr Leu Arg Ala Asn Gly Ala Asp Val  
 390 395 400 405  
 gat tac agg cgt ttg tat gcg ttc tat atc aat tac acg ata ggt ttt 1482  
 Asp Tyr Arg Arg Leu Tyr Ala Phe Tyr Ile Asn Tyr Thr Ile Gly Phe  
 410 415 420  
 taagctcttt ttagggctta taaagaggct ttttactttt tttttggtat tctaacaagc 1542  
 ttttaaataa tccaatctac tttgttttaa ggataatatt ttatggcaga tgctgttggtg 1602  
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 gactt 1667

<210> 84  
 <211> 421  
 <212> PRT  
 <213> *Helicobacter pylori*

<400> 84  
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 Gly Val Gly Met Ala Gly Gly Asn Gly Leu Leu Ala Leu Ala Thr Asn  
 35 40 45  
 Thr Thr Met Asp Ala Leu Leu Gly Ile Gly Asn Gln Ile Val Asn Thr  
 50 55 60  
 Asn Thr Thr Val Ser Asn Asn Ala Glu Leu Thr Gln Phe Lys Lys  
 65 70 75 80  
 Ile Leu Pro Gln Ile Glu Gln Arg Phe Glu Thr Asn Lys Asn Ala Tyr  
 85 90 95  
 Ser Val Gln Ala Leu Gln Val Tyr Leu Ser Asn Val Leu Tyr Asn Leu  
 100 105 110  
 Val Asn Asn Ser Asn Asn Gly Ser Asn Asn Gly Val Val Pro Glu Tyr  
 115 120 125  
 Val Gly Ile Ile Lys Val Leu Tyr Gly Ser Gln Asn Glu Phe Ser Leu  
 130 135 140  
 Leu Ala Thr Glu Ser Val Val Leu Leu Asn Ala Leu Thr Arg Val Asn  
 145 150 155 160  
 Leu Asp Ser Asn Ser Val Phe Leu Lys Gly Leu Leu Ala Gln Met Gln  
 165 170 175  
 Leu Phe Asn Asp Thr Ser Ser Ala Lys Leu Gly Gln Ile Ala Glu Asn  
 180 185 190  
 Leu Lys Asn Gly Gly Ala Gly Ser Met Leu Gln Lys Asp Val Lys Thr  
 195 200 205  
 Ile Ser Asp Arg Ile Ala Thr Tyr Gln Glu Asn Leu Lys Gln Leu Gly

210		215		220
Gly Met Leu Lys Asn Tyr Asp Glu Pro Tyr Leu Pro Gln Phe Gly Pro				
225		230		235
Gly Thr Ser Ser Gln His Gly Val Ile Asn Gly Phe Gly Ile Gln Val				
	245		250	
Gly Tyr Lys Gln Phe Phe Gly Asn Lys Arg Asn Ile Gly Leu Arg Tyr				
	260	265		270
Tyr Ala Phe Phe Asp Tyr Gly Phe Thr Gln Leu Gly Ser Leu Ser Ser				
	275	280		285
Ala Val Lys Ala Asn Ile Phe Thr Tyr Gly Ala Gly Thr Asp Phe Leu				
	290	295		300
Trp Asn Ile Phe Arg Arg Val Phe Ser Asp Gln Ser Leu Asn Val Gly				
305		310		315
Val Phe Gly Gly Ile Gln Ile Ala Gly Asn Thr Trp Asp Ser Ser Leu				
	325		330	
Arg Gly Gln Ile Glu Asn Ser Phe Lys Glu Tyr Pro Thr Pro Thr Asn				
	340	345		350
Phe Gln Phe Leu Phe Asn Leu Gly Leu Arg Ala His Phe Ala Ser Thr				
	355	360		365
Met His Arg Arg Phe Leu Ser Ala Ser Gln Ser Ile Gln His Gly Met				
	370	375		380
Glu Phe Gly Val Lys Ile Pro Ala Ile Asn Gln Arg Tyr Leu Arg Ala				
385		390		395
Asn Gly Ala Asp Val Asp Tyr Arg Arg Leu Tyr Ala Phe Tyr Ile Asn				
	405	410		415
Tyr Thr Ile Gly Phe				
	420			

<210> 85  
 <211> 926  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (207)...(746)

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 gcatttgcaa gaaactttga tgatagaagt ggaaggcctt gatttttctt tagtgagcgc 180  
 cttgaacatt ttagcgcgca tggaga atg aaa agc atg cgt ttt agt tac att 233  
 Met Lys Ser Met Arg Phe Ser Tyr Ile

	1		5	
gag cca aga gcg aaa tac ctt atc agc aag ctt tct aaa att tgg gtt				281
Glu Pro Arg Ala Lys Tyr Leu Ile Ser Lys Leu Ser Lys Ile Trp Val				
10	15	20	25	

ttt tac att ttt tta tct ttt gtg gta ata ggg ggg tta gtg tgg ttt				329
Phe Tyr Ile Phe Leu Ser Phe Val Val Ile Gly Gly Leu Val Trp Phe				
	30	35	40	

atg cac aac gcc att aaa agc act caa gac aac gcg tcc agt ttg acg				377
Met His Asn Ala Ile Lys Ser Thr Gln Asp Asn Ala Ser Ser Leu Thr				
	45	50	55	

atc caa gaa agg ctc tac cgc cat gaa atc agc cgc tta cag gtt aag				425
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Ile	Gln	Glu	Arg	Leu	Tyr	Arg	His	Glu	Ile	Ser	Arg	Leu	Gln	Val	Lys		
		60					65					70					
act	gat	gaa	acc	tta	aaa	ctc	att	aaa	gaa	gcc	aaa	aag	cgt	ttg	aat	473	
Thr	Asp	Glu	Thr	Leu	Lys	Leu	Ile	Lys	Glu	Ala	Lys	Lys	Arg	Leu	Asn		
		75				80				85							
tat	aac	gat	gat	ata	cga	gat	gtt	ttg	caa	ggg	ctt	ttg	aat	att	gtg	521	
Tyr	Asn	Asp	Asp	Ile	Arg	Asp	Val	Leu	Gln	Gly	Leu	Leu	Asn	Ile	Val		
		90			95				100						105		
cgc	gat	tcc	atc	act	att	aat	agc	att	gaa	ata	gac	cag	caa	agc	gtg	569	
Pro	Asp	Ser	Ile	Thr	Ile	Asn	Ser	Ile	Glu	Ile	Asp	Gln	Gln	Ser	Val		
				110					115					120			
gtt	gtt	agc	ggg	aaa	acc	cct	tct	aaa	gaa	gcc	ttt	tat	ttt	ttg	ttt	617	
Val	Val	Ser	Gly	Lys	Thr	Pro	Ser	Lys	Glu	Ala	Phe	Tyr	Phe	Leu	Phe		
			125					130					135				
caa	aac	aaa	cta	aac	ccc	atg	ttt	gat	tat	tct	agg	gcg	gaa	ttt	ttc	665	
Gln	Asn	Lys	Leu	Asn	Pro	Met	Phe	Asp	Tyr	Ser	Arg	Ala	Glu	Phe	Phe		
		140					145					150					
ccc	tta	agc	gat	ggg	tgg	ttt	aat	ttt	gtc	tcc	acc	aac	ttt	tct	aat	713	
Pro	Leu	Ser	Asp	Gly	Trp	Phe	Asn	Phe	Val	Ser	Thr	Asn	Phe	Ser	Asn		
		155				160					165						
tcc	tta	ctg	ata	aaa	aat	ccg	gag	tct	att	aaa	tgaagccatt	gcattttttca	766				
Ser	Leu	Leu	Ile	Lys	Asn	Pro	Glu	Ser	Ile	Lys							
		170			175				180								
cacctggaca	gagagcaatc	aggcgatgtg	gggtttatca	ttaaaaacct	cgtttttttta	826											
gggggtttttt	ccttattggg	ttggttgaat	accgagtatt	ttctatggcc	tagcatgctg	886											
gaattaaaaa	aaatcctttt	agaagaaaat	cgtaaaaaaa			926											

<210> 86  
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 <212> PRT  
 <213> Helicobacter pylori

<400> 86

Met	Lys	Ser	Met	Arg	Phe	Ser	Tyr	Ile	Glu	Pro	Arg	Ala	Lys	Tyr	Leu		
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Ile	Ser	Lys	Leu	Ser	Lys	Ile	Trp	Val	Phe	Tyr	Ile	Phe	Leu	Ser	Phe		
			20					25					30				
Val	Val	Ile	Gly	Gly	Leu	Val	Trp	Phe	Met	His	Asn	Ala	Ile	Lys	Ser		
		35				40					45						
Thr	Gln	Asp	Asn	Ala	Ser	Ser	Leu	Thr	Ile	Gln	Glu	Arg	Leu	Tyr	Arg		
	50				55					60							
His	Glu	Ile	Ser	Arg	Leu	Gln	Val	Lys	Thr	Asp	Glu	Thr	Leu	Lys	Leu		
	65				70				75					80			
Ile	Lys	Glu	Ala	Lys	Lys	Arg	Leu	Asn	Tyr	Asn	Asp	Asp	Ile	Arg	Asp		
			85					90					95				
Val	Leu	Gln	Gly	Leu	Leu	Asn	Ile	Val	Pro	Asp	Ser	Ile	Thr	Ile	Asn		
		100						105					110				
Ser	Ile	Glu	Ile	Asp	Gln	Gln	Ser	Val	Val	Val	Ser	Gly	Lys	Thr	Pro		
		115				120						125					
Ser	Lys	Glu	Ala	Phe	Tyr	Phe	Leu	Phe	Gln	Asn	Lys	Leu	Asn	Pro	Met		
		130				135					140						

Phe Asp Tyr Ser Arg Ala Glu Phe Phe Pro Leu Ser Asp Gly Trp Phe  
 145 150 155 160  
 Asn Phe Val Ser Thr Asn Phe Ser Asn Ser Leu Leu Ile Lys Asn Pro  
 165 170 175  
 Glu Ser Ile Lys  
 180

<210> 87  
 <211> 1440  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (151)...(1299)

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 aacgatgagg tgagcgatgc gtttttaatc atacaagatt ttaaagaaca gcgcatacatt 120  
 cataaaatca ttcaaaccga tttcaaacgc atg tgc gtg gtt ttg agc gtg aaa 174  
 Met Cys Val Val Leu Ser Val Lys  
 1 5

aga gat ggt gaa aaa act tta gaa aat aat gaa gaa aat aaa gat gaa 222  
 Arg Asp Gly Glu Lys Thr Leu Glu Asn Asn Glu Glu Asn Lys Asp Glu  
 10 15 20

aag ctt att ttg att gat gaa ttt gaa gtt tta gcc aat aaa ttc att 270  
 Lys Leu Ile Leu Ile Asp Glu Phe Glu Val Leu Ala Asn Lys Phe Ile  
 25 30 35 40

tct cgt ttg ccc aat atc cct agc acc cct aga gag ttt ggg tta ggc 318  
 Ser Arg Leu Pro Asn Ile Pro Ser Thr Pro Arg Glu Phe Gly Leu Gly  
 45 50 55

aag ggc gag atc atg gag att gat gtg cct ttt ggg agt att ttt gct 366  
 Lys Gly Glu Ile Met Glu Ile Asp Val Pro Phe Gly Ser Ile Phe Ala  
 60 65 70

tac aga cac att ggc tct atc aga caa aaa gaa tac agg att gta ggg 414  
 Tyr Arg His Ile Gly Ser Ile Arg Gln Lys Glu Tyr Arg Ile Val Gly  
 75 80 85

ctt tat cgc aac gat gtt ttg ttg ctc tcc act aaa tct tta gtt atc 462  
 Leu Tyr Arg Asn Asp Val Leu Leu Leu Ser Thr Lys Ser Leu Val Ile  
 90 95 100

cag ccg cga gac att ctc tta gtg gcg ggt aat ccg gaa att ttg aat 510  
 Gln Pro Arg Asp Ile Leu Leu Val Ala Gly Asn Pro Glu Ile Leu Asn  
 105 110 115 120

gcg gtg tat ctt caa gtc aaa agc aat gtg ggg cag ttc cca gcc ccc 558  
 Ala Val Tyr Leu Gln Val Lys Ser Asn Val Gly Gln Phe Pro Ala Pro  
 125 130 135

ttt ggt aag agc att tat tta tac att gat atg cgt ttg cag aac aga 606  
 Phe Gly Lys Ser Ile Tyr Leu Tyr Ile Asp Met Arg Leu Gln Asn Arg  
 140 145 150



aaa gcg atg atg cgc gat gtg tat caa gcc ttg ttt ttg cac aaa cat	654
Lys Ala Met Met Arg Asp Val Tyr Gln Ala Leu Phe Leu His Lys His	
155 160 165	
tta aag agc tac aag ctc tac att cag gtt tta cac ccc act agc cct	702
Leu Lys Ser Tyr Lys Leu Tyr Ile Gln Val Leu His Pro Thr Ser Pro	
170 175 180	
aag ttt tac cat aaa ttt tta gcg cta gaa acc gaa agc att gaa gtg	750
Lys Phe Tyr His Lys Phe Leu Ala Leu Glu Thr Glu Ser Ile Glu Val	
185 190 195 200	
aat ttt gat ttt tac agg aaa agt ttt atc caa aaa ctc cat gaa gac	798
Asn Phe Asp Phe Tyr Arg Lys Ser Phe Ile Gln Lys Leu His Glu Asp	
205 210 215	
cac cag aaa aaa atg ggc cta atc gtg gta ggc aga gag ctt ttt tta	846
His Gln Lys Lys Met Gly Leu Ile Val Val Gly Arg Glu Leu Phe Leu	
220 225 230	
tct aaa aaa cac cga aag gcc ttg tat aaa aca gcc acc cca gtt tat	894
Ser Lys Lys His Arg Lys Ala Leu Tyr Lys Thr Ala Thr Pro Val Tyr	
235 240 245	
aaa acc aac act tct ggc ttg tct aaa acc tct caa agc gtg gtg gta	942
Lys Thr Asn Thr Ser Gly Leu Ser Lys Thr Ser Gln Ser Val Val Val	
250 255 260	
ttg aat gaa agt ttg gat att aat gag gac atg tct tca gtg att ttt	990
Leu Asn Glu Ser Leu Asp Ile Asn Glu Asp Met Ser Ser Val Ile Phe	
265 270 275 280	
gat gtg tct atg caa atg gat ttg ggc ttg ttg ctc tat gat ttt gac	1038
Asp Val Ser Met Gln Met Asp Leu Gly Leu Leu Leu Tyr Asp Phe Asp	
285 290 295	
cct aac aag cgc tat aaa aac gag att gtc aat cat tat gaa aat tta	1086
Pro Asn Lys Arg Tyr Lys Asn Glu Ile Val Asn His Tyr Glu Asn Leu	
300 305 310	
gcc aac gcg ttc aac cgc aag att gag att ttc caa acc gat att aga	1134
Ala Asn Ala Phe Asn Arg Lys Ile Glu Ile Phe Gln Thr Asp Ile Arg	
315 320 325	
aat cct atc atg tat ctc aat tct tta aga aat ccc att ttg cat ttc	1182
Asn Pro Ile Met Tyr Leu Asn Ser Leu Arg Asn Pro Ile Leu His Phe	
330 335 340	
atg cct ttt gaa gag tgc atc acg cac acg cgc ttt tgg tgg ttt tta	1230
Met Pro Phe Glu Glu Cys Ile Thr His Thr Arg Phe Trp Trp Phe Leu	
345 350 355 360	
tcc act aaa gtg gaa aaa tta gcg ttt tta aac gat gat aac cct caa	1278
Ser Thr Lys Val Glu Lys Leu Ala Phe Leu Asn Asp Asp Asn Pro Gln	
365 370 375	
att ttt atc cct gta gcg gag tgaaagaatg caagaaattt taatcccttt	1329
Ile Phe Ile Pro Val Ala Glu	

aaaagaaaaa aactataaag tgtttttggg ggaactgcct gaaataaaat tgaaacaaaa 1389  
 agccctcatc attagcgata gcatcgtagc cgggttgcat ttgccctatt t 1440

<210> 88

<211> 383

<212> PRT

<213> *Helicobacter pylori*

<400> 88

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Asn	Asn	Glu	Glu	Asn	Lys	Asp	Glu	Lys	Leu	Ile	Leu	Ile	Asp	Glu	Phe
		20					25						30		
Glu	Val	Leu	Ala	Asn	Lys	Phe	Ile	Ser	Arg	Leu	Pro	Asn	Ile	Pro	Ser
		35					40					45			
Thr	Pro	Arg	Glu	Phe	Gly	Leu	Gly	Lys	Gly	Glu	Ile	Met	Glu	Ile	Asp
	50					55					60				
Val	Pro	Phe	Gly	Ser	Ile	Phe	Ala	Tyr	Arg	His	Ile	Gly	Ser	Ile	Arg
65					70					75					80
Gln	Lys	Glu	Tyr	Arg	Ile	Val	Gly	Leu	Tyr	Arg	Asn	Asp	Val	Leu	Leu
				85					90					95	
Leu	Ser	Thr	Lys	Ser	Leu	Val	Ile	Gln	Pro	Arg	Asp	Ile	Leu	Leu	Val
			100					105					110		
Ala	Gly	Asn	Pro	Glu	Ile	Leu	Asn	Ala	Val	Tyr	Leu	Gln	Val	Lys	Ser
		115					120					125			
Asn	Val	Gly	Gln	Phe	Pro	Ala	Pro	Phe	Gly	Lys	Ser	Ile	Tyr	Leu	Tyr
	130					135					140				
Ile	Asp	Met	Arg	Leu	Gln	Asn	Arg	Lys	Ala	Met	Met	Arg	Asp	Val	Tyr
145					150					155					160
Gln	Ala	Leu	Phe	Leu	His	Lys	His	Leu	Lys	Ser	Tyr	Lys	Leu	Tyr	Ile
				165					170					175	
Gln	Val	Leu	His	Pro	Thr	Ser	Pro	Lys	Phe	Tyr	His	Lys	Phe	Leu	Ala
		180						185					190		
Leu	Glu	Thr	Glu	Ser	Ile	Glu	Val	Asn	Phe	Asp	Phe	Tyr	Arg	Lys	Ser
		195					200					205			
Phe	Ile	Gln	Lys	Leu	His	Glu	Asp	His	Gln	Lys	Lys	Met	Gly	Leu	Ile
	210					215					220				
Val	Val	Gly	Arg	Glu	Leu	Phe	Leu	Ser	Lys	Lys	His	Arg	Lys	Ala	Leu
225					230					235					240
Tyr	Lys	Thr	Ala	Thr	Pro	Val	Tyr	Lys	Thr	Asn	Thr	Ser	Gly	Leu	Ser
				245					250					255	
Lys	Thr	Ser	Gln	Ser	Val	Val	Val	Leu	Asn	Glu	Ser	Leu	Asp	Ile	Asn
			260					265					270		
Glu	Asp	Met	Ser	Ser	Val	Ile	Phe	Asp	Val	Ser	Met	Gln	Met	Asp	Leu
		275					280					285			
Gly	Leu	Leu	Leu	Tyr	Asp	Phe	Asp	Pro	Asn	Lys	Arg	Tyr	Lys	Asn	Glu
	290					295					300				
Ile	Val	Asn	His	Tyr	Glu	Asn	Leu	Ala	Asn	Ala	Phe	Asn	Arg	Lys	Ile
305					310					315					320
Glu	Ile	Phe	Gln	Thr	Asp	Ile	Arg	Asn	Pro	Ile	Met	Tyr	Leu	Asn	Ser
				325					330					335	
Leu	Arg	Asn	Pro	Ile	Leu	His	Phe	Met	Pro	Phe	Glu	Glu	Cys	Ile	Thr
			340					345					350		
His	Thr	Arg	Phe	Trp	Trp	Phe	Leu	Ser	Thr	Lys	Val	Glu	Lys	Leu	Ala
		355					360					365			
Phe	Leu	Asn	Asp	Asp	Asn	Pro	Gln	Ile	Phe	Ile	Pro	Val	Ala	Glu	
	370					375					380				



Met	Val	Gly	Gly	Gly	Thr	Val	Lys	Lys	Asp	Leu	Lys	Lys	Ala	Ile	Gln
1				5					10					15	
Tyr	Tyr	Val	Lys	Ala	Cys	Glu	Leu	Asn	Glu	Met	Phe	Gly	Cys	Leu	Ser
		20						25					30		
Leu	Val	Ser	Asn	Ser	Gln	Ile	Asn	Lys	Gln	Lys	Leu	Phe	Gln	Tyr	Leu
		35					40					45			
Ser	Lys	Ala	Cys	Glu	Leu	Asn	Ser	Gly	Asn	Gly	Cys	Arg	Phe	Leu	Gly
	50					55					60				
Asp	Phe	Tyr	Glu	Asn	Gly	Lys	Tyr	Val	Lys	Lys	Asp	Leu	Arg	Lys	Ala
65					70					75					80
Ala	Gln	Tyr	Tyr	Ser	Lys	Ala	Cys	Gly	Leu	Asn	Asp	Gln	Asp	Gly	Cys
				85					90					95	
Leu	Ile	Leu	Gly	Tyr	Lys	Gln	Tyr	Ala	Gly	Lys	Gly	Val	Val	Lys	Asn
			100					105					110		
Glu	Lys	Gln	Ala	Val	Lys	Thr	Phe	Glu	Lys	Ala	Cys	Arg	Leu	Gly	Ser
		115					120					125			
Glu	Asp	Ala	Cys	Gly	Ile	Leu	Asn	Asn	Tyr						
	130					135									

<210> 91  
 <211> 1663  
 <212> DNA  
 <213> *Helicobacter pylori*

<220>  
 <221> CDS  
 <222> (68)...(1600)

<400> 91  
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 aacaaac atg aaa aaa ctt ctt tat acc ata ctc gcg ctt ctt tta atc 109  
     Met Lys Lys Leu Leu Tyr Thr Ile Leu Ala Leu Leu Ile  
     1                    5                    10

ggc ctt tta aca atc tat ctc atc ctt ttt aca gaa tgg ggg aat aag 157  
 Gly Leu Leu Thr Ile Tyr Leu Ile Leu Phe Thr Glu Trp Gly Asn Lys  
     15                    20                    25                    30

atc atc gct tcg tat ata gag aaa aaa atc aac ccg aac gag cac tac 205  
 Ile Ile Ala Ser Tyr Ile Glu Lys Lys Ile Asn Pro Asn Glu His Tyr  
                     35                    40                    45

ttg agc gtt aaa acc ttt aaa ttg aga ttc aac tct ttg gat ttt aaa 253  
 Leu Ser Val Lys Thr Phe Lys Leu Arg Phe Asn Ser Leu Asp Phe Lys  
                     50                    55                    60

gct caa gcc aac gat gat tcc acg ctc att ctt aag ggg gat ttt tca 301  
 Ala Gln Ala Asn Asp Asp Ser Thr Leu Ile Leu Lys Gly Asp Phe Ser  
                     65                    70                    75

ctt tta aag caa agc gta aat ttg aat tac cat ata gat att aaa gat 349  
 Leu Leu Lys Gln Ser Val Asn Leu Asn Tyr His Ile Asp Ile Lys Asp  
     80                    85                    90

tta cgc tct ttc aaa gaa tgg ata ccc tac cct tta agg ggg gct gtt 397  
 Leu Arg Ser Phe Lys Glu Trp Ile Pro Tyr Pro Leu Arg Gly Ala Val  
     95                    100                    105                    110

atc act tct ggg aat att aaa ggg cat aga aaa gcc ctt atg att caa	445
Ile Thr Ser Gly Asn Ile Lys Gly His Arg Lys Ala Leu Met Ile Gln	
115 120 125	
ggc gtc tct aat gtg gct caa tcc cac act gcc tac aat gcc ctt tta	493
Gly Val Ser Asn Val Ala Gln Ser His Thr Ala Tyr Asn Ala Leu Leu	
130 135 140	
gat gat ttc aag ctt tct cgc tta aat ttg aac gca caa gac gcc aat	541
Asp Asp Phe Lys Leu Ser Arg Leu Asn Leu Asn Ala Gln Asp Ala Asn	
145 150 155	
tta gaa gat ttg ctt tat tta atc aat cgc ccc gct tat gcg aac gca	589
Leu Glu Asp Leu Leu Tyr Leu Ile Asn Arg Pro Ala Tyr Ala Asn Ala	
160 165 170	
aaa gtg tcc tta cag gcg gat ttt aac tct cta aag cct tta gag ggg	637
Lys Val Ser Leu Gln Ala Asp Phe Asn Ser Leu Lys Pro Leu Glu Gly	
175 180 185 190	
cat ttg atc cta aca gct aat aac gct tta atc aat aac gcc cta atc	685
His Leu Ile Leu Thr Ala Asn Asn Ala Leu Ile Asn Asn Ala Leu Ile	
195 200 205	
aat caa att ttt cat tta aac ctt aaa gac acg ctt gtt ttc agc ctc	733
Asn Gln Ile Phe His Leu Asn Leu Lys Asp Thr Leu Val Phe Ser Leu	
210 215 220	
tcg cat tca agc gac ttt aaa gga aac aaa gcc atc agc gat acc acc	781
Ser His Ser Ser Asp Phe Lys Gly Asn Lys Ala Ile Ser Asp Thr Thr	
225 230 235	
ctg act agc cct tta gcc aat ttc aaa gcc cta aaa agc gaa tac ctt	829
Leu Thr Ser Pro Leu Ala Asn Phe Lys Ala Leu Lys Ser Glu Tyr Leu	
240 245 250	
ttc tct att tta aaa ctc aac gcc ccc tac act tta gaa atc ccc aat	877
Phe Ser Ile Leu Lys Leu Asn Ala Pro Tyr Thr Leu Glu Ile Pro Asn	
255 260 265 270	
cta gcc aaa ctc tat aac att acc aac cac ccc tta aaa ggg agc ttg	925
Leu Ala Lys Leu Tyr Asn Ile Thr Asn His Pro Leu Lys Gly Ser Leu	
275 280 285	
act tta aaa ggc gct ata gaa caa agc ccc aaa ctt tta aaa gtc agc	973
Thr Leu Lys Gly Ala Ile Glu Gln Ser Pro Lys Leu Leu Lys Val Ser	
290 295 300	
ggc cat tca aat tta cta gac ggc gcg ctg gat ttc acg ctt tta aat	1021
Gly His Ser Asn Leu Leu Asp Gly Ala Leu Asp Phe Thr Leu Leu Asn	
305 310 315	
aaa gat ttg aaa ggg cgt ttt tcc aat att tcc act tta aaa gct tta	1069
Lys Asp Leu Lys Gly Arg Phe Ser Asn Ile Ser Thr Leu Lys Ala Leu	
320 325 330	
gat tta ttc cat tac cct aag ttt ttc caa tcc gtt gca gac gct aat	1117
Asp Leu Phe His Tyr Pro Lys Phe Phe Gln Ser Val Ala Asp Ala Asn	
335 340 345 350	

ttg gat tat gat ctt atc gct aag caa ggc gta ttg aaa gcc cgc cta 1165  
 Leu Asp Tyr Asp Leu Ile Ala Lys Gln Gly Val Leu Lys Ala Arg Leu  
 355 360 365

aaa aac gca aga ttc ctc aaa aat gca ttc agc gat ttt ctc tac tcc 1213  
 Lys Asn Ala Arg Phe Leu Lys Asn Ala Phe Ser Asp Phe Leu Tyr Ser  
 370 375 380

att tct aaa ttt gat att aca aaa gaa att tat aac gat gcc aat ctg 1261  
 Ile Ser Lys Phe Asp Ile Thr Lys Glu Ile Tyr Asn Asp Ala Asn Leu  
 385 390 395

gta agc caa atc aac cag caa cgc ctg ctc tct gat ctg agt tta aaa 1309  
 Val Ser Gln Ile Asn Gln Gln Arg Leu Leu Ser Asp Leu Ser Leu Lys  
 400 405 410

agc ccc aaa acc caa ttg aaa atc cat aac ggt ttg ttg gat tta aac 1357  
 Ser Pro Lys Thr Gln Leu Lys Ile His Asn Gly Leu Leu Asp Leu Asn  
 415 420 425 430

acc aaa caa atg aac atg ctc atg gat gcg gaa att tta aaa ttc att 1405  
 Thr Lys Gln Met Asn Met Leu Met Asp Ala Glu Ile Leu Lys Phe Ile  
 435 440 445

ttt aaa atg aaa ctt caa ggc aac atg cac cag cca aaa ttt tct ctc 1453  
 Phe Lys Met Lys Leu Gln Gly Asn Met His Gln Pro Lys Phe Ser Leu  
 450 455 460

att tta aac gaa aaa gcc att cag caa aac ttg caa caa ggc ttg aaa 1501  
 Ile Leu Asn Glu Lys Ala Ile Gln Gln Asn Leu Gln Gln Gly Leu Lys  
 465 470 475

gaa atc tta aaa aac gac acc ctt aaa aaa ggt tta gat cat ttg ctt 1549  
 Glu Ile Leu Lys Asn Asp Thr Leu Lys Lys Gly Leu Asp His Leu Leu  
 480 485 490

aaa gat gat aag ctc aaa gaa aag ctt gaa aaa ggg ctt aag ggg ctt 1597  
 Lys Asp Asp Lys Leu Lys Glu Lys Leu Glu Lys Gly Leu Lys Gly Leu  
 495 500 505 510

ttt taataatttt aaaggataga aatggcgac attttagtta gcggggcgac 1650  
 Phe

ttcagggttt gga 1663

<210> 92

<211> 511

<212> PRT

<213> Helicobacter pylori

<400> 92

Met Lys Lys Leu Leu Tyr Thr Ile Leu Ala Leu Leu Leu Ile Gly Leu

1 5 10 15

Leu Thr Ile Tyr Leu Ile Leu Phe Thr Glu Trp Gly Asn Lys Ile Ile

20 25 30

Ala Ser Tyr Ile Glu Lys Lys Ile Asn Pro Asn Glu His Tyr Leu Ser

35 40 45

Val	Lys	Thr	Phe	Lys	Leu	Arg	Phe	Asn	Ser	Leu	Asp	Phe	Lys	Ala	Gln
50						55					60				
Ala	Asn	Asp	Asp	Ser	Thr	Leu	Ile	Leu	Lys	Gly	Asp	Phe	Ser	Leu	Leu
65					70					75					80
Lys	Gln	Ser	Val	Asn	Leu	Asn	Tyr	His	Ile	Asp	Ile	Lys	Asp	Leu	Arg
				85					90					95	
Ser	Phe	Lys	Glu	Trp	Ile	Pro	Tyr	Pro	Leu	Arg	Gly	Ala	Val	Ile	Thr
			100					105					110		
Ser	Gly	Asn	Ile	Lys	Gly	His	Arg	Lys	Ala	Leu	Met	Ile	Gln	Gly	Val
		115				120						125			
Ser	Asn	Val	Ala	Gln	Ser	His	Thr	Ala	Tyr	Asn	Ala	Leu	Leu	Asp	Asp
	130					135					140				
Phe	Lys	Leu	Ser	Arg	Leu	Asn	Leu	Asn	Ala	Gln	Asp	Ala	Asn	Leu	Glu
145					150					155					160
Asp	Leu	Leu	Tyr	Leu	Ile	Asn	Arg	Pro	Ala	Tyr	Ala	Asn	Ala	Lys	Val
				165					170					175	
Ser	Leu	Gln	Ala	Asp	Phe	Asn	Ser	Leu	Lys	Pro	Leu	Glu	Gly	His	Leu
			180					185					190		
Ile	Leu	Thr	Ala	Asn	Asn	Ala	Leu	Ile	Asn	Asn	Ala	Leu	Ile	Asn	Gln
		195				200						205			
Ile	Phe	His	Leu	Asn	Leu	Lys	Asp	Thr	Leu	Val	Phe	Ser	Leu	Ser	His
	210					215					220				
Ser	Ser	Asp	Phe	Lys	Gly	Asn	Lys	Ala	Ile	Ser	Asp	Thr	Thr	Leu	Thr
225					230					235					240
Ser	Pro	Leu	Ala	Asn	Phe	Lys	Ala	Leu	Lys	Ser	Glu	Tyr	Leu	Phe	Ser
				245					250					255	
Ile	Leu	Lys	Leu	Asn	Ala	Pro	Tyr	Thr	Leu	Glu	Ile	Pro	Asn	Leu	Ala
			260					265					270		
Lys	Leu	Tyr	Asn	Ile	Thr	Asn	His	Pro	Leu	Lys	Gly	Ser	Leu	Thr	Leu
		275					280					285			
Lys	Gly	Ala	Ile	Glu	Gln	Ser	Pro	Lys	Leu	Leu	Lys	Val	Ser	Gly	His
	290					295					300				
Ser	Asn	Leu	Leu	Asp	Gly	Ala	Leu	Asp	Phe	Thr	Leu	Leu	Asn	Lys	Asp
305					310					315					320
Leu	Lys	Gly	Arg	Phe	Ser	Asn	Ile	Ser	Thr	Leu	Lys	Ala	Leu	Asp	Leu
				325					330					335	
Phe	His	Tyr	Pro	Lys	Phe	Phe	Gln	Ser	Val	Ala	Asp	Ala	Asn	Leu	Asp
			340					345					350		
Tyr	Asp	Leu	Ile	Ala	Lys	Gln	Gly	Val	Leu	Lys	Ala	Arg	Leu	Lys	Asn
	355					360						365			
Ala	Arg	Phe	Leu	Lys	Asn	Ala	Phe	Ser	Asp	Phe	Leu	Tyr	Ser	Ile	Ser
	370					375					380				
Lys	Phe	Asp	Ile	Thr	Lys	Glu	Ile	Tyr	Asn	Asp	Ala	Asn	Leu	Val	Ser
385					390					395					400
Gln	Ile	Asn	Gln	Gln	Arg	Leu	Leu	Ser	Asp	Leu	Ser	Leu	Lys	Ser	Pro
				405					410					415	
Lys	Thr	Gln	Leu	Lys	Ile	His	Asn	Gly	Leu	Leu	Asp	Leu	Asn	Thr	Lys
			420					425					430		
Gln	Met	Asn	Met	Leu	Met	Asp	Ala	Glu	Ile	Leu	Lys	Phe	Ile	Phe	Lys
		435					440					445			
Met	Lys	Leu	Gln	Gly	Asn	Met	His	Gln	Pro	Lys	Phe	Ser	Leu	Ile	Leu
	450				455						460				
Asn	Glu	Lys	Ala	Ile	Gln	Gln	Asn	Leu	Gln	Gln	Gly	Leu	Lys	Glu	Ile
465					470					475					480
Leu	Lys	Asn	Asp	Thr	Leu	Lys	Lys	Gly	Leu	Asp	His	Leu	Leu	Lys	Asp
				485					490					495	
Asp	Lys	Leu	Lys	Glu	Lys	Leu	Glu	Lys	Gly	Leu	Lys	Gly	Leu	Phe	
			500					505					510		

<210> 93  
 <211> 947  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (292) ... (645)

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ccatgcctct atcacgcctt taaatttaga ctttaaccagt tatgatgatt tgaaaagttt 180
ggaatcttgg catgagggaa tgttaaagtg agtaaaaagc accgcttggc ttttttaggg 240
ctaattgttg gggttctatt cttcttttagt gcgtgtgagc accgcctgca c atg ggg 297
                                         Met Gly
                                         1

tat tat tca gaa gtt aca ggg gat tat ttg ttc aat tat aat tcc act 345
Tyr Tyr Ser Glu Val Thr Gly Asp Tyr Leu Phe Asn Tyr Asn Ser Thr
      5              10              15

atc gtg gtg gct tat gac aga agc gat gcg atg act tct tat tat atc 393
Ile Val Val Ala Tyr Asp Arg Ser Asp Ala Met Thr Ser Tyr Tyr Ile
      20              25              30

aat gtg att gtt tat gaa ttg caa aaa tta ggc ttt tac aat gtc ttc 441
Asn Val Ile Val Tyr Glu Leu Gln Lys Leu Gly Phe Tyr Asn Val Phe
      35              40              45

acg caa gcg gaa ttc cca cta gat aaa gcc aaa aat gtg atc tat gcg 489
Thr Gln Ala Glu Phe Pro Leu Asp Lys Ala Lys Asn Val Ile Tyr Ala
      55              60              65

cgc att gtc cgt aac atc tca gct gtg ccg ttc tac caa tac aat tac 537
Arg Ile Val Arg Asn Ile Ser Ala Val Pro Phe Tyr Gln Tyr Asn Tyr
      70              75              80

caa ctg att gat caa gtc aat aag cct tgt tat ttt ctt ggg ggg cag 585
Gln Leu Ile Asp Gln Val Asn Lys Pro Cys Tyr Phe Leu Gly Gly Gln
      85              90              95

ttt tat tgc tct caa acc cta cgg att att acg cta tca atg gct tta 633
Phe Tyr Cys Ser Gln Thr Leu Arg Ile Ile Thr Leu Ser Met Ala Leu
      100              105              110

gcg agc aaa ttt taatgagtgc taattcgcat tttatttttag attggtatga 685
Ala Ser Lys Phe
115

tgtggtgttg caaaaacggg ttttatatgt ggatgggagc gtgagcggga ggacttgcg 745
ctatcagatg ctgtataggg atttgattaa aagcacgac aaacgcattg attttaaccg 805
ccctgaacgc tactactaca atttaagact gcccttttat cagccatgtt ataggcaatg 865
aaatggttat caggcgattg tatcaatttt gcgctagcca tgtggtgcgc aattgctctt 925
ctttaaaatg cgctcaaaat at                                     , 947

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<210> 94  
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<400> 94

<210> 95

<211> 875

<212> DNA

 $\langle 220 \rangle$ 

<221> CDS

 $\langle 222 \rangle \quad (348) \dots (716)$ 

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Phe Lys Ser Val Ser Ala Ile Lys Lys Asp Glu Asn Ile Thr Ala Asn  
5 10 15

aac act caa aaa gag cgc att ttg ttt ggt gcg ctt tct aac ccc tta 452  
Asn Thr Gln Lys Glu Arg Ile Leu Phe Gly Ala Leu Ser Asn Pro Leu  
20 25 30 35

tta gag ggc gcg att gat aaa gtg agc gcg aaa aat ttt atc ccc cct 500  
Leu Glu Gly Ala Ile Asp Lys Val Ser Ala Lys Asn Phe Ile Pro Pro  
40 45 50

aac acg ctt tta agc acg gat aaa acc caa gct tta att atc gtg cgt 548  
Asn Thr Leu Leu Ser Thr Asp Lys Thr Gln Ala Leu Ile Ile Val Arg  
55 60 65

aaa aat gac att atc acc ggg gtg tat gaa gag ggg caa atc agc ata 596  
Lys Asn Asp Ile Ile Thr Gly Val Tyr Glu Glu Gly Gln Ile Ser Ile  
70 75 80

gaa ata agc cta aaa gcc cta gaa aat ggc gcg ctt aat caa atc att 644  
 Glu Ile Ser Leu Lys Ala Leu Glu Asn Gly Ala Leu Asn Gln Ile Ile  
           85                                  90                                  95

caa gcg aaa aat tta gaa agc aat aaa ata ctc aaa gca aaa gtg ttg 692  
 Gln Ala Lys Asn Leu Glu Ser Asn Lys Ile Leu Lys Ala Lys Val Leu  
 100                                  105                                  110                                  115

agc agc tct aaa gcg caa atc tta taaaggacat tcatgaaatt ggttttaggc 746  
 Ser Ser Ser Lys Ala Gln Ile Leu  
                                   120

atcagtggag cgagcgggat acccctagcc ttgcggtttt tagaaaaatt acccaaagaa 806  
 attgaagttt ttgtcgtggc gtctaaaaac gcgcatgtcg tggcgttaga agaattctaat 866  
 attaacctt 875

<210> 96  
 <211> 123  
 <212> PRT  
 <213> Helicobacter pylori

<400> 96  
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 Thr Ala Asn Asn Thr Gln Lys Glu Arg Ile Leu Phe Gly Ala Leu Ser  
                                   20                                  25                                  30  
 Asn Pro Leu Leu Glu Gly Ala Ile Asp Lys Val Ser Ala Lys Asn Phe  
                                   35                                  40                                  45  
 Ile Pro Pro Asn Thr Leu Leu Ser Thr Asp Lys Thr Gln Ala Leu Ile  
   50                                  55                                  60  
 Ile Val Arg Lys Asn Asp Ile Ile Thr Gly Val Tyr Glu Glu Gly Gln  
 65                                  70                                  75                                  80  
 Ile Ser Ile Glu Ile Ser Leu Lys Ala Leu Glu Asn Gly Ala Leu Asn  
                                   85                                  90                                  95  
 Gln Ile Ile Gln Ala Lys Asn Leu Glu Ser Asn Lys Ile Leu Lys Ala  
                                   100                                  105                                  110  
 Lys Val Leu Ser Ser Ser Lys Ala Gln Ile Leu  
                                   115                                  120

<210> 97  
 <211> 394  
 <212> DNA  
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 <221> CDS  
 <222> (160)...(345)

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 aaagatttat cccagaaga attggaaaat taaaaacgc atg caa aaa gaa caa 174  
                                   Met Gln Lys Glu Gln  
                                   1                                  5

gaa gcc caa gaa atc gct aaa aaa gcc gtt aaa atc gtg ttt ttt tta 222  
 Glu Ala Gln Glu Ile Ala Lys Lys Ala Val Lys Ile Val Phe Phe Leu

10 15 20  
 ggg ctt gtg gtg gtg ctt ttg atg atg ata aac ctt tac atg ctc atc 270  
 Gly Leu Val Val Val Leu Leu Met Met Ile Asn Leu Tyr Met Leu Ile  
 25 30 35  
 aat caa atc aac gcg agc gct caa atg agc cac caa atc aaa aag ata 318  
 Asn Gln Ile Asn Ala Ser Ala Gln Met Ser His Gln Ile Lys Lys Ile  
 40 45 50  
 gaa gaa agg ctt aat cag gag caa aaa taaaaaaggc tttttggtat 365  
 Glu Glu Arg Leu Asn Gln Glu Gln Lys  
 55 60

ttttacgatc aaatagtaaa gagcttattc 394

<210> 98  
 <211> 62  
 <212> PRT  
 <213> Helicobacter pylori

<400> 98  
 Met Gln Lys Glu Gln Glu Ala Gln Glu Ile Ala Lys Lys Ala Val Lys  
 1 5 10 15  
 Ile Val Phe Phe Leu Gly Leu Val Val Val Leu Leu Met Met Ile Asn  
 20 25 30  
 Leu Tyr Met Leu Ile Asn Gln Ile Asn Ala Ser Ala Gln Met Ser His  
 35 40 45  
 Gln Ile Lys Lys Ile Glu Glu Arg Leu Asn Gln Glu Gln Lys  
 50 55 60

<210> 99  
 <211> 516  
 <212> DNA  
 <213> Helicobacter pylori

<400> 99  
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 agaaaaggcg cagttgtttt aatgcgtttg tttatcgcg tagttttgtt ttggtggtgg 120  
 ttaagcttga acgctaaaga agcggatttt atctctgatt tagaatcgg gatggctctt 180  
 tataaaaacc ctagggtgtg tgcgtgcgcg aaatgccatg gcattaaagg cgaacaacaa 240  
 gaaatcacct tttattatga aaaaggcgag aaaaaaatcc tctacgcccc taaaatcaac 300  
 catttggtt ttaaaacctt taaagacgcc ttgagtttag gcaaaggcat gatgcctaaa 360  
 tacaatctca atttagaaga aatccaagcg atttatcttt atatcatctc tttagagcat 420  
 aaagaagagc gtaaggattc tcctaagcct taatcaaagc gcttgattta tgctaaaatg 480  
 gagcgttgca tttttgtttt gattaaagaa gggttc 516

<210> 100  
 <211> 709  
 <212> DNA  
 <213> Helicobacter pylori

<400> 100  
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 aggagcctaa ctaaaataaa atgaacaatt tcagttaggg ctttattata gcaaaaatta 180  
 tctaagatta caaagggtag cgtttctgtt tttggattta gagcgttatt ttgattgttt 240  
 tgagtttaatt ttactttttg ttttaataata aatcctaact atcataaatg tacaattaaa 300

gtattttaaaa	aaatttttaaa	acaaaaggat	ataaaatgaa	aaccattaga	aatagcgtgt	360
ttattggagc	gtcttttactc	ggcggttgcg	ctagcgttga	ggcttatttt	gacgctttgc	420
atgttgctcg	cgttaaagac	gcttgtttat	agaaaaagaa	gcacaccaca	cgcccaaaga	480
ctttgatagc	ccttaccaca	ctgactaaac	cggcactagg	ttttagttgg	gggttttttag	540
gggtgttatt	ttagatactc	tctgttcctt	taaagaaaat	aaatttctac	cataaaataa	600
aatcttaaat	taaggcgact	aaaacccac	ttttaaaaaa	ttaaaaagcg	ttaagtaaga	660
cttatccaaa	aagcaaagaa	aatcaatttt	tccaaccact	ttttttaag		709

<210> 101

<211> 33

<212> DNA

<213> Helicobacter pylori

<400> 101

cgcggatccg	aaatagggtt	gtttttaatt	ttc	33
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<210> 102

<211> 30

<212> DNA

<213> Helicobacter pylori

<400> 102

ccgctcgagt	taaaaaaaga	gtttgtataa	30
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<210> 103

<211> 25

<212> DNA

<213> Helicobacter pylori

<400> 103

ggggatcctt	ggtagaattg	aatca	25
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<210> 104

<211> 23

<212> DNA

<213> Helicobacter pylori

<400> 104

ggaattccta	aaacaagaac	gcg	23
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<210> 105

<211> 25

<212> DNA

<213> Helicobacter pylori

<400> 105

ggggatcctt	ttttcaaaaa	caata	25
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<210> 106

<211> 23

<212> DNA

<213> Helicobacter pylori

<400> 106

ggaattctca	cattgttttg	ctc	23
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<210> 107

<211> 23

<212> DNA

<213> Helicobacter pylori  
 <400> 107  
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 <210> 108  
 <211> 25  
 <212> DNA  
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 <400> 108  
 ccgctcgaac taaaaactat aaacg 25  
 <210> 109  
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 <400> 109  
 cgcgatccg agattttgaa aggttggtta tg 32  
 <210> 110  
 <211> 30  
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 <400> 110  
 ccgctcgagc tacatccttt tactataacc 30  
 <210> 111  
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 <400> 111  
 gcggatccgg gtattattca gaag 24  
 <210> 112  
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 <212> DNA  
 <213> Helicobacter pylori  
 <400> 112  
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